A scoping review of viral diseases in African ungulates

By

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Declaration

I, Hendrik Johannes Swanepoel, declare that the work presented in this dissertation, which I hereby submit for the degree Magister Scientiae (Tropical Animal Health) at the Department of Veterinary Tropical Diseases, Faculty of Veterinary Science, University of Pretoria, South Africa was executed by me under the supervision of Professor Melvyn Quan and the co-supervision of Dr Jannie Crafford. This is the first presentation of this work for degree compliance at this or any other tertiary institution, sources of information have been acknowledged accordingly.

10/06/2020

Date

Signature

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A scoping review of viral diseases in African ungulates

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Rationale: Viral diseases are important in the African context as they cause significant clinical disease in both wild and domestic animals, as well as in humans. Viral diseases make up a large proportion of emerging infectious diseases. The management and prevention of these diseases have proven to be challenging due to the large population of reservoir hosts consisting of African wildlife. There is no comprehensive publication investigating viruses in African ungulates. Hence, this research study will provide comprehensive analyses to add to the current global knowledge base and provide guidance about areas where there is little information.

Aim of the study: Provide a scoping review of viral diseases, which occur in free-ranging African ungulates and identify knowledge gaps with regards to these diseases.

Objectives:

1. List and describe viruses diagnosed in free-ranging African ungulates
2. Identify ungulates affected by viruses
3. Describe the geographical distribution of viruses
4. Identify viruses which appear to be “under-studied”

Study design: This is a scoping review of peer reviewed publications pertaining to viruses and viral diseases in African ungulates. The methodology for this scoping review was based on the guidelines set out in the PRISMA extension for scoping reviews. A search string was developed and run in three major databases, namely Scopus, Web of Science and Wildlife and Ecology Worldwide, to obtain publications relevant to the research topic. Publications were screened using predetermined inclusion and exclusion criteria to obtain a final set of publications to undergo data extraction and analysis.

Results: The final set of publications consisted of 145 publications. A total of 32 viruses were identified in the publications. The range of the publication dates were from 1957 to 2018. Nine out of 32 viruses accounted for 74% of the total reports of viruses detected by antigen/antibody testing in African ungulates. *African elephant polyomavirus 1* was the only virus that was solely detected in captive animals according to published literature using antigen/antibody detection. A total of 50 African ungulates were reported/diagnosed with viral infections. The four most frequently mentioned African ungulates in publications reporting on viruses or viral diseases, in descending order, were the African buffalo, blue wildebeest, impala and warthog (common and desert). Of the 52 countries on the African continent, only 18 countries (35%) had viruses diagnosed in wild ungulates reported in the literature. All the publications in this study reported on viruses or viral diseases in ungulates from only sub-Saharan Africa. Foot-and-mouth disease, African swine fever, Rift Valley fever, bluetongue and rabies were frequently reported in the literature. On the contrary, lumpy skin disease, peste des petits ruminants, African horse sickness, enzootic hemorrhagic disease, bovine viral diarrhoea, infectious bovine rhinotracheitis/infectious pustular vulvovaginitis, equine influenza, equine viral arteritis, equine viral rhinopneumonitis and classical swine fever were infrequently reported on.

Conclusion: There are a variety of viruses which have been diagnosed in African ungulates and all African ungulates identified have had one or more viruses or viral diseases associated with them. The findings will be valuable to policymakers, funding bodies, researchers and other stakeholders who need an understanding of viral diseases in African ungulates. Research opportunities in this field will allow them to make informed decisions about investment in future research projects and animal health policies and protocols. It is recommended that governments and research institutions offer more funding to investigate and report viral diseases of greater clinical and zoonotic significance, such as rabies and Rift Valley fever. This is especially important in the current climate of emerging diseases and the related overflow of disease from wild to domestic animals and from animals, both wild and domestic, to humans. A further recommendation is for appropriate One Health approaches to be adopted for investigating, controlling, managing and preventing diseases (Cunningham *et al.*, 2017). This is especially true for diseases such as African swine fever and Rift Valley fever where human actions, poor biosecurity and natural weather changes play a major role in the transmission of diseases (Cunningham *et al.*, 2017, Penrith *et al.*, 2019a, Swanepoel and Coetzer, 2004). Diseases which may threaten the conservation of certain wildlife species also require focused attention. In order to keep track of these diseases it may be necessary to consider adding a “wildlife” category to the OIE-listed diseases.

Viral diseases, as a whole, are of great significance and require extra attention in the future as they make up a large proportion of emerging infectious diseases and can often infect

multiple hosts (Bengis *et al.*, 2004, Cleaveland *et al.*, 2001). Hence, the viruses and viral diseases diagnosed in African ungulates are of significance, particularly at the wildlife/livestock interface and many of them have the potential of becoming emerging wildlife diseases.

2. INTRODUCTION

2.1. RATIONALE

Viral diseases are important in the African context as they cause significant clinical disease in both wild and domestic animals, as well as in humans. Viral diseases make up a large proportion of emerging infectious diseases. The management and prevention of these diseases have proven to be challenging due to the large population of reservoir hosts consisting of African wildlife.

The past few decades have seen some diseases emerge, and re-emerge, and the impact of these diseases on human and animal health has been catastrophic. Emerging infectious diseases pose a significant threat to global public health and a large percentage (> 60%) are zoonotic (Cleaveland *et al.*, 2001, Epstein *et al.*, 2006). Emerging diseases have become more important because of growing populations of human beings and domestic animals, culminating in a surge of emergence of zoonotic diseases (Cunningham *et al.*, 2017, Jones *et al.*, 2008). Furthermore, some diseases which were once geographically isolated are now becoming global disease issues and threats due to the ease of travel and trade in animals and animal products (Cunningham *et al.*, 2017, Karesh *et al.*, 2005). Emerging diseases are of particular importance in developing countries as they have a profound negative impact on food security and the livelihoods of poverty-stricken people. In addition, emerging diseases pose a major economic burden in both developing and developed countries as large amounts of money need to be spent in order to prevent disease emergence and maintain ongoing surveillance for emerging diseases (Cunningham *et al.*, 2017, Daszak *et al.*, 2000).

Viral diseases are of great significance as they make up a large proportion of emerging infectious diseases (Cleaveland *et al.*, 2001, Cunningham *et al.*, 2017). Furthermore, viral diseases are of particular importance in the African context as many of them affect more than one species of animal and pose a significant threat to entire ecosystems as biodiversity, animal behaviour and animal population composition can be affected. As a result, some species have even been pushed to the brink of extinction by several factors, including viral diseases (Cunningham *et al.*, 2017, Daszak *et al.*, 2000). The management and prevention of these diseases have proven to be challenging due to the large population of reservoir hosts consisting of African wildlife (Bengis *et al.*, 2002, Kock, 2005). In South Africa, the wildlife industry forms a major part of both the agricultural and tourism sectors and contributes greatly to the country's economy (Taylor *et al.*, 2016). This industry suffers both direct (mortality and reduced productivity) and indirect losses (management and prevention costs, trade losses,

reduced value of animals and food insecurity) due to infectious diseases (Wiethoelter *et al.*, 2015).

Wildlife and the specific diseases infecting them are often neglected in studies and wild animals are rather categorised according to their epidemiological role as hosts, usually spillover, maintenance or dead-end hosts (Cleaveland *et al.*, 2001). There have been a large number of studies investigating specific viral diseases and numerous diseases of significance have been identified (Bengis *et al.*, 2002, Kock, 2005).

There are several viruses known to cause clinical disease in African ungulates and a proportion of these viruses have been diagnosed only in captive-bred wildlife. The aim of this study is to identify those viruses which have been detected in free-ranging wildlife. The viral diseases known to be present in African wildlife include, but are not limited to, foot-and-mouth disease (FMD), rabies, African horse sickness (AHS), African swine fever (ASF), Rift Valley fever (RVF), bluetongue, lumpy skin disease (LSD), malignant catarrhal fever (MCF), encephalomyocarditis of elephants (EMC), peste des petits ruminants (PPR), canine distemper and feline immunodeficiency syndrome (Bengis *et al.*, 2002).

The pathogens which form the basis of this paper are viruses which have been isolated in African ungulates. This excludes domestic (e.g. sheep, cattle, goats and pigs) and feral ungulates (e.g. camels).

There is no comprehensive publication reviewing the publications on viruses in African ungulates. This research study aimed to fill this gap and provide comprehensive analyses to add to the current global knowledge base and provide guidance about areas lacking knowledge.

2.2. AIM

Provide a scoping review of viral diseases, which occur in free-ranging African ungulates and identify knowledge gaps with regards to these diseases.

2.3. OBJECTIVES

1. List and describe viruses diagnosed in free-ranging African ungulates.
2. Identify ungulates affected by viruses.
3. Describe the geographical distribution of viruses.
4. Identify viruses which appear to be “under-studied”.

2.4. RESEARCH TOPIC AND QUESTIONS

The study consisted of a scoping review. At the start of the study, a team of experts in the fields of microbiology, research and data gathering was established. This team constructed the topic of the study as well as the study protocol, which included the databases to be searched and the development of search strings.

The population, interest and context (PICO) framework was modified and used to develop the research topic and questions. The population in focus being African ungulates, the interest being viral diseases of these animals and the context being to establish what the current global knowledge base is and to identify gaps in the knowledge base (Wiethoelter *et al.*, 2015).

“Knowledge synthesis” denotes the integration of results obtained from individual research studies pertaining to a specific disease, topic or question into the global knowledge base (Young *et al.*, 2014). A scoping review is the most suitable method of knowledge synthesis by which existing knowledge is mapped to areas in the global knowledge base where a lack of comprehensive analyses exist (Arksey and O'Malley, 2005, Levac *et al.*, 2010, Munn *et al.*, 2018).

Knowledge synthesis methodologies were applied in this paper to deliver a comprehensive overview of published research on viral diseases of African ungulates. The intention was to quantitatively characterise peer-reviewed research with respect to the author, date of publication, reference type, animal species involved, virus involved, how the disease was diagnosed, and temporal and regional patterns to establish the focus of research on viral diseases and to identify any gaps. The study aimed to answer specific research questions:

1. Which viruses have been diagnosed in African ungulates?
2. Which African ungulates have had viruses or viral diseases diagnosed?
3. What is the geographical distribution of these viruses and their diseases?
4. Which diseases are “under-studied”?

2.5. OVERVIEW OF VIRAL DISEASES

2.5.1. Adenoviridae

2.5.1.1. Bovine mastadenovirus infection

Bovine mastadenovirus (Genus: *Mastadenovirus*, Family: *Adenoviridae*) (ICTV, 2019) most commonly causes disease of the gastrointestinal and respiratory tracts of wild and domestic

bovids. Animals may become persistently infected and usually shed the virus in respiratory secretions and faeces (Baber and Condy, 1981).

2.5.2. Arteriviridae

2.5.2.1. Equine viral arteritis

Equine viral arteritis (EVA) is an acute infectious disease of equids caused by *Alphaarterivirus equid* (AAE) (Genus: *Alphaarterivirus*, Family: *Arteriviridae*) (ICTV, 2019). EVA is present globally and may cause vague clinical signs, such as lethargy, inappetence, pyrexia and abortions in pregnant mares. It can cause a state of persistent subclinical infection in stallions but not in mares or geldings (Borchers *et al.*, 2005). Antibodies against AAE have been detected in wild ungulates but the virus does not seem to cause clinical disease in wild animals (Barnard, 1997, Borchers *et al.*, 2005).

2.5.3. Asfarviridae

2.5.3.1. African swine fever

African swine fever virus (ASFV) (Genus: *Asfivirus*, Family: *Asfarviridae*) (ICTV, 2019) only infects species of the *Suidae* family and there is no vaccine or treatment for infected pigs (Anderson *et al.*, 1998, Penrith *et al.*, 2013, Penrith *et al.*, 2019a). It was first identified around 1920 in Kenya where studies were conducted to investigate a pig disease, epidemiologically and immunologically different from classical swine fever (Penrith *et al.*, 2019a). ASFV causes a disease characterised by haemorrhagic fever and can have mortality rates of up to 100% in domestic pigs (Penrith *et al.*, 2019a, Zhou *et al.*, 2018). The main wild reservoir of ASFV is the warthog (*Phacocoerus spp.*), and evidence of infection with ASFV of bushpigs (*Potamochoerus larvatus*) and giant forest hogs (*Hylochoerus meinertzhageni*) exists but the degree of infection and the role of these wild suids in the epidemiology of ASF is unknown (Anderson *et al.*, 1998, Penrith *et al.*, 2019a). The African swine fever control zone in South Africa consists of the northern sections of the North-West and KwaZulu-Natal provinces and the Limpopo province north of Bela-Bela; in this zone warthogs are considered infected and are reservoirs of ASFV, despite some warthog burrows not harbouring the tampan vector (Wilkinson *et al.*, 1988). Recent outbreaks south of this zone in Gauteng and the Free State suggests that the epidemiology of African swine fever is changing (Swanepoel, B. pers. comm.).

2.5.4. Flaviviridae

2.5.4.1. Classical swine fever

Classical swine fever (CSF) is an acute haemorrhagic disease of suids caused by *Pestivirus C* (Genus: *Pestivirus*, Family: *Flaviviridae*) (ICTV, 2019) (Everett *et al.*, 2011). CSF commonly infects domestic swine and causes disease of varying severity and mortality. Some pigs can recover from infection and become immune. Disease caused by CSF in wild African suids (warthog and bushpig) has only been reported under experimental conditions (Everett *et al.*, 2011).

2.5.4.2. Pestivirus A/B infection

Many domestic ungulates, including cattle, sheep, goats and pigs, as well as wild ungulates, both in captive and free-ranging situations, can be infected with *Pestivirus A/B*, formerly known as *bovine viral diarrhea virus* (BVDV) (Genus: *Pestivirus*, Family: *Flaviviridae*) (ICTV, 2019). Little is known about the health effects of *Pestivirus A/B* on wild African ungulates and the seroprevalence of *Pestivirus A/B* in wild African ungulates (Scott *et al.*, 2013). A high prevalence of infection with *Pestivirus A/B* in herds of buffalo and wildebeest has been reported (Nettleton, 1990) and there is evidence that *Pestivirus A/B* may cause clinical disease in several wild ruminant species including kudu, eland, giraffe, buffalo and deer (Scott *et al.*, 2013, Hamblin and Hedger, 1979).

2.5.4.3. Wesselsbron disease

Wesselsbron disease is a zoonotic disease caused by *Wesselsbron virus* (Genus: *Flavivirus*, Family: *Flaviviridae*) (ICTV, 2019), which is transmitted by mosquitoes and causes acute disease in domestic ruminants, mainly in sub-Saharan Africa. It may cause mortalities in young animals and usually results in subclinical disease in adult animals; however, mortality may also occur (Weyer *et al.*, 2013). Antibodies against *Wesselsbron virus* have been detected in wild ungulates, but the virus does not seem to cause clinical disease in wild animals (Barnard, 1997).

2.5.5. Herpesviridae

2.5.5.1. Bovine alpha- and gammaherpesvirus infections

Bovine alpha- and *gammaherpesvirus* (Genus: *Macavirus*/*Simplexvirus*/*Rhadinovirus*/ *Varicellovirus*, Family: *Herpesviridae*) (ICTV, 2019) cause a variety of clinical signs of disease,

including neurological, respiratory and reproductive and sometimes neurological disease, in both domestic and wild bovids (Dewals *et al.*, 2005, Dewals *et al.*, 2006).

2.5.5.2. Elephantid herpesvirus infection

Elephantid betaherpesvirus (Genus: *Proboscivirus*, Family: *Herpesviridae*) (ICTV, 2019) has been detected in wild and captive elephant populations (Bronson *et al.*, 2017). It has been suggested that the virus originated in African elephants (*Loxodonta africana*). When African and Asian elephants (*Elephas maximus*) are kept in close proximity to each other, the disease can be transmitted to Asian elephants with fatal consequences. However, current evidence suggests that multiple herpesviruses that co-evolved with elephant populations, circulate naturally within these populations and get shed intermittently (Bronson *et al.*, 2017, Long *et al.*, 2016, Zong *et al.*, 2014). Twelve strains of elephant herpesvirus have been identified. These strains likely occur in various populations of free-ranging African elephants. Several of these strains of herpesvirus have been linked to fatal endotheliolytic disease, in both African and Asian elephants (Long *et al.*, 2016).

2.5.5.3. Equid herpesvirus infection

Equid herpesviruses (Genus: *Percavirus/Varicellovirus*, Family: *Herpesviridae*) (ICTV, 2019) cause a variety of clinical signs of disease, including neurological, respiratory and reproductive disease, in both domestic and wild equids. Nine herpesviruses that infect equids have been identified (Abdelgawad *et al.*, 2015).

2.5.5.4. Malignant catarrhal fever

There are two main variants of MCF: they are caused by the sheep-associated *Ovine gammaherpesvirus 2* (Genus: *Macavirus*, Family: *Herpesviridae*) and wildebeest-associated *Alcelaphine gammaherpesvirus 1* and *2* (Genus: *Macavirus*, Family: *Herpesviridae*) (ICTV 2019) (Hussain *et al.*, 2017). Large numbers of domestic and wild ruminants have been reported to develop clinical signs associated with MCF (Wambua *et al.*, 2016). Furthermore, many different species of wild ruminants in captivity are susceptible to infection by both types of virus (Ortiz *et al.*, 2018). To date, clinical cases of MCF have not been reported in free-ranging wild African ungulates, but cases have been reported in semi-captive African buffalo kept in close proximity to sheep (Pfitzer *et al.*, 2015). MCF is readily transmitted from blue and black wildebeest to cattle in conditions where they live in close proximity to each other, such as in semi-captive conditions (Hussain *et al.*, 2017, Pfitzer *et al.*, 2015). Several surveillance studies have found antibodies against wildebeest-associated MCF from several antelope

species. However, there is currently no evidence that these species transmit the disease to cattle under natural conditions (Pfitzer *et al.*, 2015).

2.5.6. Papillomaviridae

2.5.6.1. Bovine papilloma

Deltapapillomavirus 4 (Genus: *Papillomavirus*, Family: *Papillomaviridae*) (ICTV, 2019), known previously as *bovine papillomavirus 1*, commonly causes self-limiting wart-like lesions on the skin and gastrointestinal tract of cattle and less commonly can cause more significant neoplastic lesions of the gastrointestinal tract and urinary bladder of cattle (van Dyk *et al.*, 2011, van Dyk *et al.*, 2009). Significant clinical disease has been reported in wild ungulates, namely giraffe and sable antelope (van Dyk *et al.*, 2011). Interestingly, papillomavirus is not host-specific and causes significant skin disease in the form of sarcoid like lesions in domestic equids as well as free-ranging zebras (van Dyk *et al.*, 2009).

2.5.7. Paramyxoviridae

2.5.7.1. Bovine respirovirus infection

Bovine respirovirus 3 (Genus: *Respirovirus*, Family: *Paramyxoviridae*) (ICTV, 2019), previously known as *bovine parainfluenza virus 3*, commonly causes a subclinical infection in cattle. It will usually only cause clinical respiratory disease when co-infection with other pathogens (viral and/or bacterial) occur and when animals undergo significant amounts of stress (Grissett *et al.*, 2015). Antibodies to *bovine respirovirus 3* have been isolated in various wild African ungulates, including African buffalo, wildebeest, hippopotamus, elephant, rhinoceros, zebra, giraffe and several species of antelope (Barnard, 1997, Fischer-Tenhagen *et al.*, 2000, Hamblin and Hedger, 1978).

2.5.7.2. Rinderpest

Rinderpest morbillivirus (Genus: *Morbillivirus*, Family: *Paramyxoviridae*) (ICTV, 2019) caused rinderpest which, on 25 May 2011 was declared eradicated at the General Assembly of the World Organisation for Animal Health (OIE) in Paris, France. The method of eradication was mainly by means of effective vaccination campaigns, part of intensive management strategies implemented by several countries and international organisations over a number of decades. Rinderpest represented the first animal viral disease successfully eradicated globally (Morens *et al.*, 2011). It has been included in this scoping review for completeness.

2.5.7.3. Peste des petits ruminants

Small ruminant morbillivirus (SRM), previously known as *peste des petits ruminants virus* (PPRV) (Genus: *Morbillivirus*, Family: *Paramyxoviridae*) (ICTV, 2019) is a viral infection causing peste des petits ruminants (PPR), a severe respiratory disease of small ruminants and it occurs in many countries across the globe (Albina *et al.*, 2013, Munir, 2014, Schulz *et al.*, 2018). The disease is of major economic and transboundary significance (Munir, 2014). African buffalo developed antibodies to the virus, but do not show signs of disease (Albina *et al.*, 2013). However, the virus does cause morbidity and mortality in other wild ruminants, e.g. duiker (Ogunsanmi *et al.*, 2003). SRM is present across most of the African continent (Schulz *et al.*, 2018). There is a vaccine available against SRM but given the widespread nature of SRM and the variety of wild hosts, the control and management of the disease is particularly challenging, especially where wildlife and domestic small ruminants come into contact with each other (Albina *et al.*, 2013, Munir, 2014). A One Health approach to the management of SRM will provide the best outcome and may lead to SRM being the next eradicated infectious disease, following rinderpest (Albina *et al.*, 2013).

2.5.8. Peribunyaviridae

2.5.8.1. Akabane disease

Akabane orthobunyavirus (Genus: *Orthobunyavirus*, Family: *Peribunyaviridae*) (ICTV, 2019) is transmitted by biting insects, such as midges. It does not cause clinical disease in adult animals but can cause congenital abnormalities of ruminant foetuses (Fischer-Tenhagen *et al.*, 2000). Clinical disease caused by *Akabane orthobunyavirus* has not been reported in wild African ruminants but antibodies to the virus have been detected (Barnard, 1997, Fischer-Tenhagen *et al.*, 2000, Hamblin *et al.*, 1990). The highest antibody titres were detected in black and white rhinoceros, which, according to the authors, suggests that these animals may be susceptible to infection (Fischer-Tenhagen *et al.*, 2000).

2.5.9. Phenuiviridae

2.5.9.1. Rift Valley fever

Rift Valley fever phlebovirus (RVFP) (Genus: *Phlebovirus*, Family: *Phenuiviridae*) (ICTV, 2019) is transmitted by mosquitoes and haematophagous flies and causes clinical disease in a wide range of mammals, including humans. It was first identified in 1930 during a disease epidemic in sheep in the Rift Valley of Kenya (Beechler *et al.*, 2015). It has the potential to become a global emerging infectious disease (Beechler *et al.*, 2015, Fagbo *et al.*, 2014,

Swanepoel and Coetzer, 2004). African buffalo and some antelope species have a low prevalence of antibodies to RVFP, with minimal evidence of clinical disease. RVFP is endemic in tropical regions of Africa with high annual rainfall (Beechler *et al.*, 2015). Clinical cases of RVF have been reported in free-ranging wildlife and it is believed that a significant challenge with high concentrations of the virus may cause clinical disease (Beechler *et al.*, 2015, Manore and Beechler, 2015). However, clinical disease in free-ranging wildlife remains an irregular event and despite multiple outbreaks and ongoing research, there has not yet been any concrete evidence to implicate a mammalian reservoir host of RVFP (Rostal *et al.*, 2017). Mosquitoes, on the other hand, seem to act as maintenance vectors during inter-epidemic periods (Swanepoel and Coetzer, 2004). In 2006, an outbreak of RVF occurred in Kenya and in 2010 a major RVF outbreak occurred in South Africa. During these outbreaks, deaths of sable, kudu, springbok and deer were documented (Evans *et al.*, 2008, Pienaar and Thompson, 2013).

2.5.10. Picornaviridae

2.5.10.1. Foot-and-mouth disease

Foot-and-mouth disease virus (FMDV) (Genus: *Aphthovirus*, Family: *Picornaviridae*) (ICTV, 2019) causes an acute infectious disease, which infects even-toed ungulates and camels (Grubman and Baxt, 2004). The only free-ranging wild animal that is known to be capable of sustaining FMD for indeterminate periods of time is the African buffalo (Michel and Bengis, 2012). There are wide varieties of other cloven-hoofed wildlife species that become infected sporadically with FMDV, but there is little evidence to indicate that they play a role in disease transmission to livestock and disease maintenance (Weaver *et al.*, 2013). The exception to this statement may be impala in the Kruger National Park (South Africa) because there are regular outbreaks of FMD in this species. However, there is evidence to show that infected impala shed relatively small quantities of virus for short periods and FMDV does not persist in the impala population during inter-epidemic periods (Bastos *et al.*, 2000, Keet *et al.*, 1996). African buffalo play a major role in the epidemiology of FMD as the species is the free-ranging reservoir host for FMDV in sub-Saharan Africa (Ayebazibwe *et al.*, 2010, Gainaru *et al.*, 1986). FMD is of major economic importance as it affects the majority of African livestock and livestock product export markets. An outbreak of FMD can cause the export of a country to shut down, resulting in the loss of millions of dollars in revenue (Brückner *et al.*, 2002).

2.5.10.2. Encephalomyocarditis of elephants

Encephalomyocarditis (EMC) is an acute viral disease, which affects a large spectrum of animal species and the characteristic signs associated with disease are cardiac failure and/or encephalomyelitis (Lamglait *et al.*, 2015). *Cardiovirus A* (Genus: *Cardiovirus*, Family: *Picornaviridae*) (ICTV, 2019) has a global distribution (Grobler *et al.*, 1995). Rodents are the natural sylvatic reservoir hosts of *Cardiovirus A* and they excrete the virus in their urine and faeces (Grobler *et al.*, 1995). *Cardiovirus A* has been implicated in the periodic mortalities of groups of elephants in the Kruger National Park, South Africa (Lamglait *et al.*, 2015, van Sandwyk *et al.*, 2013). It is thought that elephants acquire the virus when they eat entire tufts of grass contaminated with rodent excrement. Horizontal transmission between elephants is highly unlikely to occur (Grobler *et al.*, 1995). Clinical signs of EMC in elephants are non-specific and may be similar to signs associated with septicaemia, other viral disease (*elephantid betaherpesvirus*) or cardiotoxic plants (Lamglait *et al.*, 2015). It is usually identified as the cause of death in elephants, via post-mortem examination of deceased elephants and viral isolation. It is unlikely to affect wild elephant populations in the long-term (Grobler *et al.*, 1995).

2.5.11. Poxviridae

2.5.11.1. Lumpy skin disease

Lumpy skin disease virus (LSDV) (Genus: *Capripoxvirus*, Family: *Poxviridae*) (ICTV, 2019) has been reported in buffalo in Kenya based on serological testing (Davies, 1982). Suspected cases of lumpy skin disease (LSD) in Africa have been reported in gemsbok (*Oryx gazella*) in the Kimberley district of South Africa, in springbok (*Antidorcas marsupialis*) in Namibia and in Asian water buffalo (*Bubalus bubalis*) in Egypt. A confirmed case of LSD in springbok has been reported in South Africa (Coetzer *et al.*, 2018). It is currently accepted that African buffalo and free-ranging antelope species possess an innate resistance to natural infection of *lumpy skin disease virus* (Coetzer *et al.*, 2018). However, wild African ungulates may play an important role in the epidemiology of the disease (Fagbo *et al.*, 2014).

2.5.12. Reoviridae

2.5.12.1. African horse sickness

African horse sickness virus (AHSV) (Genus: *Orbivirus*, Family: *Reoviridae*) (ICTV, 2019) is transmitted by biting midges and can infect all species of equids; there is an exceptionally high mortality rate in unvaccinated domestic horses (Becker *et al.*, 2018).

Zebras are often associated with outbreaks of African horse sickness (AHS) and do not display clinical signs of disease (Becker *et al.*, 2018, Barnard *et al.*, 1995). Further research is required to clarify the implication zebras have on the epidemiology of AHS and the spread of the virus (Carpenter *et al.*, 2017). Experimental studies have shown that viraemia related to AHS can be present in zebra for up to forty days, compared to twenty-one days in horses (Barnard *et al.*, 1994). Zebras become infected with AHSV but develop a long-term humoral immunity and thus are not infectious to midges when the initial infection is removed from the system. By one year of age, most zebras will have antibodies to the majority of AHS virus serotypes. This is due to zebras occurring in AHS endemic regions. Hence, zebras are only susceptible to infection between six months of age, when maternal immunity wanes, and twelve months of age. Zebras are not classified as a significant reservoir host of AHS (Barnard, 1998).

2.5.12.2. Bluetongue

Bluetongue virus (BTV) (Genus: *Orbivirus*, Family: *Reoviridae*) (ICTV, 2019) is transmitted by *Culicoides* midges and affects a wide range of ruminant species, domestic as well as free-ranging wild ruminants (Coetzee *et al.*, 2012). In South Africa, in 1933, it was established that wild ruminants are susceptible to BTV, as a blesbok (experimentally infected with the virus) developed a subclinical infection with a viraemia high enough to infect sheep, following injection with blood from the particular blesbok (Neitz, 1933). African antelope do not develop clinical signs of disease, though they are an important reservoir of disease from which spillover into sheep flocks may occur (Coetzee *et al.*, 2012).

2.5.12.3. Equine encephalosis virus infection

Equine encephalosis virus (EEV) (Genus: *Orbivirus*, Family: *Reoviridae*) (ICTV, 2019) is a vector-borne disease, transmitted by *Culicoides* midges, closely related to AHSV and BTV (Venter *et al.*, 1999, Venter *et al.*, 2006). EEV causes severe disease in all species of equids and was confined to South Africa (Venter *et al.*, 1999). However, since 2008 there is evidence that the virus has spread to other African countries and to Israel (Oura *et al.*, 2012).

2.5.12.4. Epizootic hemorrhagic disease

Epizootic hemorrhagic disease virus (EHDV) (Genus: *Orbivirus*, Family: *Reoviridae*) (ICTV, 2019) causes severe haemorrhagic disease in ungulates, mainly in North America. In Africa, antibodies have been identified in black and white rhinoceros but the virus does not seem to cause clinical disease in free-ranging wildlife (Fischer-Tenhagen *et al.*, 2000).

2.5.13. Rhabdoviridae

2.5.13.1. Rabies

Rabies lyssavirus (Genus: *Lyssavirus*, Family: *Rhabdoviridae*) (ICTV, 2019) causes severe neurological disease in a variety of African wildlife. Canids are most commonly associated with rabies in Africa, which include the jackal, specifically the black-backed jackal (*Canis mesomelas*) and bat-eared fox (*Otocyon megalotis*). Ungulates are generally classified as incidental hosts and are less commonly affected by rabies (Scott *et al.*, 2012). However, there is an exceptional relationship between rabies and the Greater Kudu (*Tragelaphus strepsiceros*) in Namibia (Hassel *et al.*, 2018, Scott *et al.*, 2012). Rabies has a high prevalence in kudu in Namibia and a major outbreak occurred between 1978 and 1985, during which more than 50,000 animals died (Hassel *et al.*, 2018, Hiibschle and Hiibschle, 1988, Scott *et al.*, 2012).

2.5.13.2. Ephemeral fever

Ephemeral fever, also known as three-day stiff-sickness, is a common disease of domestic cattle and is caused by *bovine fever ephemerovirus* (Genus: *Ephemerovirus*, Family: *Rhabdoviridae*) (ICTV, 2019). It is an arthropod-borne disease which causes acute generalised clinical disease, characterised by pyrexia, lameness, myopathy and tremors. Infection results in high morbidity and may result in mortalities (Walker and Klement, 2015). Clinical disease has not been reported in wild African ungulates, but antibodies to the virus have been isolated in a variety of wildlife species (Barnard, 1997, Hamblin *et al.*, 1990).

3. MATERIALS AND METHODS

The methodology for this scoping review was based on the guidelines as set out in the PRISMA extension for scoping reviews. The PRISMA extension for scoping reviews was recently developed and provides standardised definitions and guidelines for scoping reviews (Tricco *et al.*, 2018). Appendix A consists of the PRISMA checklist containing information relevant to this scoping review (Tricco *et al.*, 2018). This study was conducted systematically in four main steps: firstly, the development of the research topic with relevant questions; secondly, the literature search was conducted by researching and identifying relevant publications; thirdly, screening and sorting of search results was conducted; and finally, data extraction and analyses were performed.

Ungulates were generally defined, as animals possessing hooves and belonging to the orders *Perissodactyls* (odd-toed ungulates) and *Artiodactyls* (even-toed ungulates). Elephants (*Loxodonta africana*) were classified as ungulates for completeness as they are part of the clade *Paenungulata* (sub-ungulates). African was used to describe and define the ungulates as originating from Africa and refers to non-domestic ungulates and hence, does not include indigenous domestic African cattle, sheep or goats; nor does it include feral ungulates found in Africa, e.g., camels. African ungulates, which were described as being free-ranging or captive, were included in the study and differentiated as such. For the purpose of this study, captive African ungulates were defined as ungulates, which are indigenous to Africa and have been born and bred in captivity or have been captured with the purpose to be permanently captive animals, for example, animals held in zoological collections or intensively managed operations. Animals captured and held in a *boma* facility or smaller enclosures prior to relocation or transport were not classified as captive. Furthermore, free-ranging African ungulates were defined as ungulates, which are indigenous to Africa and live free from direct human interaction and interventions for most of their lives. This includes animals in national and private game reserves and animals on game farms, as those in southern Africa, which are managed extensively. Hence, wildlife was categorised as free-ranging as long as their management was deemed extensive.

The review topic was "Viral diseases of African ungulates". The following questions were constructed:

1. Which viruses have been isolated in African ungulates?
2. Which African ungulates have had viruses or viral diseases associated with them?
3. What is the geographical distribution of these viruses and their diseases?
4. Which diseases are “under-studied” and may provide future research opportunities?

3.1. PROTOCOL

Protocol signed off by the Research Committee of the Faculty of Veterinary Science, University of Pretoria can be provided upon request.

3.2. ELIGIBILITY CRITERIA

The eligibility criteria were set by three members of the research team. The screening process was initiated by three members of the research team but due to time and geographical constraints, it was completed by one team member.

A two-stage screening process was implemented to evaluate the relevance of publications obtained during the search process.

3.3. INFORMATION SOURCES

Three major veterinary databases were used to obtain publications for this study, namely SciVerse Scopus (multidisciplinary, 1823 - present), EBSCO Wildlife and Ecology Studies Worldwide (wildlife and ecology studies, 1892 - present) and ISI Web of Science (multidisciplinary, 1900 - present).

No language, date, subject or type filters were used during the searches, which allowed for a comprehensive search and reduced limitations on publications obtained. All databases were searched using the topic search function: this searched titles, abstracts and keywords of each publication and included publications from the databases' inception to November 2019. Several publications were also obtained by performing a reverse reference search strategy on relevant references within obtained publications (Barnard and Hassel, 1981, Bastos *et al.*, 2003, Borchers *et al.*, 2005, Doyle and Heuschele, 1983, Evans *et al.*, 2008, Hamblin and Hedger, 1979, Hassel, 1982, Mansfield *et al.*, 2006, Zsak *et al.*, 2005).

The initial search was performed in January 2019. A final follow-up search of the three scientific databases was performed in November 2019 to identify any new studies published, which were relevant to viral diseases in African ungulates since January 2019.

3.4. SEARCH

A base search string was developed using terms, which were deemed relevant and descriptive of the publications required for inclusion in this scoping review. 'Africa*' was used as the geographic search term to limit results to the African continent. No other geographical

restrictions were applied. Viruses were not specifically searched for, but rather, a broad search term was developed to include any viruses or viral diseases; this was done in order to prevent the exclusion of any viruses not previously diagnosed in African ungulates. The search terms for viruses and viral diseases were 'virus OR viral'. Search terms for the indigenous African ungulates were based on the common genus names as well as the Latin genus or species names.

This base search string was adapted to meet the requirements of the individual database search engines; Appendix B contains the complete search strings. The base search string was as follows:

Africa* AND (virus OR viral) AND (loxodonta OR "african elephant" OR giraff* OR syncerus OR "african buffalo" OR "cape buffalo" OR hippopotamus OR choeropsis OR rhinoceros OR ceratotherium OR diceros OR "equus zebra" OR "equus africanus" OR grevyi OR quagga OR phacochoerus OR warthog OR potamochoerus OR bushpig OR "red river hog" OR aepyceros OR impala OR alcelaphus OR hartebees* OR connochaetes OR wildebees* OR damaliscus OR tsessebe OR bonteb* OR blesb* OR antidorcas OR springb* OR raphicerus OR steenb* OR grysbok OR tragelaphus OR kudu OR koedoe OR nyala OR bongo OR bushbuck OR bosbok OR sitatunga OR taurotragus OR eland OR hippotragus OR sable OR roan OR oryx OR gemsb* OR pelea OR rheb* OR redunca OR reedbuck OR rietbok OR "kobus ellipsiprymnus" OR waterb* OR "kobus leche" OR lechwe OR "kobus kob" OR "kobus vardonii" OR puku OR cephalophus OR sylvicapra OR philantomba OR duiker OR oreotragus OR klipspringer OR spekei OR leptoceros OR "Gazella dorcas" OR eudorcas OR nanger OR addax OR "capra nubiana" OR "nubian ibex" OR beatragus OR hirola OR ammotragus OR "barbary sheep" OR dorcatragus OR madoqua OR "dik-dik" OR okapia OR okapi OR neotragus OR "royal antelope" OR suni OR litocranius OR gerenuk OR hyemoschus OR chevrotain OR ourebia OR oribi) AND NOT (beetle OR arthropod OR oryctes OR nudivirus OR javan OR sumatran OR "one horned" OR snake OR chicken* OR human* OR Newcastle OR arabian OR tragus OR aquaculture OR waterborne)

3.4.1. Citation management

All publications obtained during the search process were imported into EndNote X8 (Clarivate Analytics, previously Thomson Reuters). Duplicate publications were removed via EndNote's automated duplicate screening process and several more duplicates were removed manually where minor differences in the title (e.g. using uppercase letters instead of lowercase letters) did not allow EndNote to detect the duplicate. All publications underwent manual title and abstract screening for relevance and then full text screening, using EndNote X8 software.

3.4.2. Inclusion and exclusion criteria

Publications were eligible to be included in the study if the full text article was written in English and if they described general or specific viruses or viral diseases in any African ungulates. Publications that reported on viruses or viral diseases in African ungulates in zoos/captivity, experimental studies, or viruses/viral diseases in vectors were handled separately. The criteria rendering a publication as excluded, were:

1. the publication discussed viruses or viral disease in domestic species, primates, rodents, bats or invasive species; or
2. the publication was a review paper.

3.5. SELECTION OF SOURCES OF EVIDENCE

3.5.1. Title and abstract relevance screening

The first screening level involved review of only the title and the abstract of publications. Publications without keywords referring to Africa or African countries, viruses or viral diseases and any of the African ungulates in their title, abstract and keywords were excluded. Irrelevant publications were obtained due to search terms having similar meanings, different truncation rules, different search algorithms and other database settings which the user did not have control over.

This allowed a large proportion of non-relevant publications to be identified and excluded, saving time, which would have been spent procuring the full text and performing full text screening of the excluded publications.

3.5.2. Full text screening

The full text of relevant publications, identified by the title and abstract screening, were obtained via several methods. Some were obtained using the full text procurement function of EndNote, which is linked to the library service of the University of Pretoria (UP). The majority were obtained by searching for the title in Google Scholar, which is also linked to the UP Library service, and directly via the UP Library services' database search function. A small number of publications required procurement by request from other university libraries, which was orchestrated by one of the team members who had expertise in research and data gathering. Some publications obtained from international university libraries were unobtainable in English and hence were excluded based on language, as access to translational services was limited.

The full text articles were screened for eligibility and if criteria were not met the publications were excluded at this step. Once the final set of full text publications was constructed, data were extracted from the publications.

3.6. DATA CHARTING PROCESS

Data extraction and charting were performed using EndNote X8 software and Microsoft Access Office 365 (Microsoft Corporation, Redmond, WA). Tables were created in the database for the data items detailed below. A data charting form was used to capture information relevant to answering the research questions and objectives (Figure 1).

3.7. DATA ITEMS

Specific data extracted from relevant studies were as follows:

1. Reference
    a. EndNote reference number, first author surname and date of publication
2. Reference type
    a. Assay (Antibody) development
    b. Assay (Antigen) development
    c. Assay (molecular) development
    d. Case/outbreak report
    e. Phylogenetic study
    f. Surveillance
    g. Experiment
3. Animal
    a. Genus
    b. Species
4. Range
    a. Free-range
    b. Captive
5. Virus
    a. Family
    b. Genus
    c. Species
6. Diagnosis
    a. Clinical signs (positive diagnosis)
    b. Laboratory - viral isolation (positive diagnosis)

c. Laboratory - antigen detection (positive diagnosis)
d. Laboratory - molecular detection (positive diagnosis)
e. Laboratory - antibody detection (positive diagnosis)
f. Clinical signs (negative diagnosis)
g. Laboratory - viral isolation (negative diagnosis)
h. Laboratory - antigen detection (negative diagnosis)
i. Laboratory - molecular detection (negative diagnosis)
j. Laboratory - antibody detection (negative diagnosis)

7. Outbreak
    a. Year of data collected, study performed, publication or outbreak/case report
8. Country
    a. Includes all African countries
9. Latitude (of outbreak)
10. Longitude (of outbreak)
11. Quantitative data (yes/no)
12. Comments

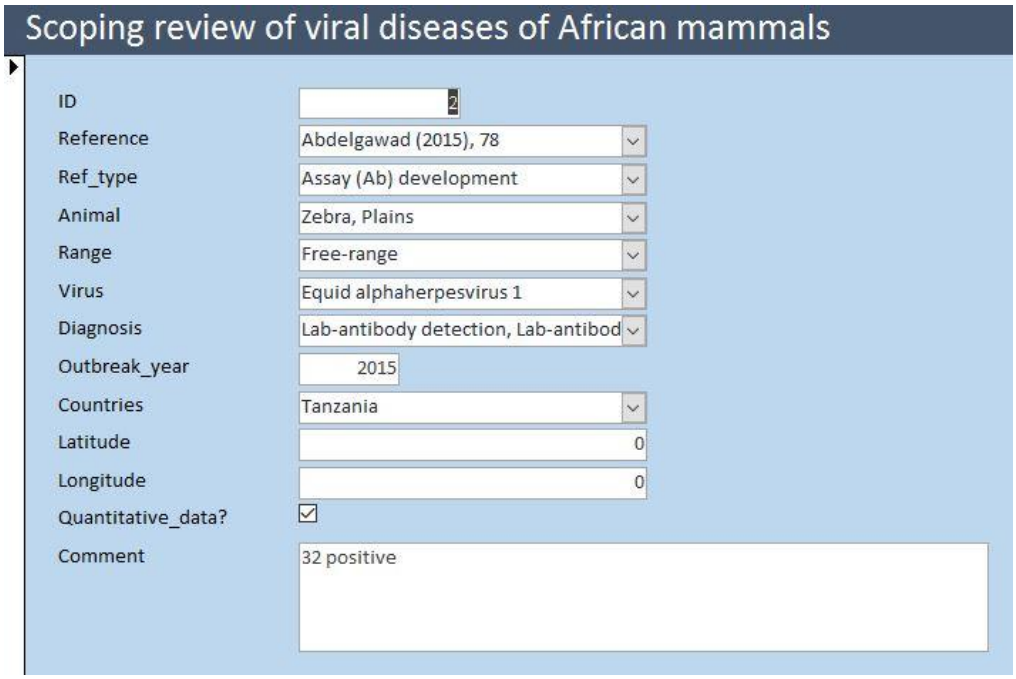


Figure 1: Screenshot of a Microsoft Access database form used to extract data from publications.

3.8. CRITICAL APPRAISAL OF INDIVIDUAL SOURCES OF EVIDENCE

A critical appraisal of each publication did not take place prior to data extraction due to time constraints.

3.9. SYNTHESIS OF RESULTS

The Microsoft Access Office 365 database allowed the construction of queries to calculate descriptive and quantitative results to summarise the data. Results were depicted as maps, graphs and plots using Microsoft Excel Office 365 (Microsoft Corporation, Redmond, WA) and ArcGIS Desktop 10.6 (Esri, USA).

4. RESULTS

4.1. SELECTION OF SOURCES OF EVIDENCE

The number of publications retrieved from each database for each of the two searches were as follows:

- Scopus
    - January 2019 - 248 publications, removed duplicates and 237 left
    - November 2019 - 11 new publications, all irrelevant
- Wildlife and Ecology Studies Worldwide
    - January 2019 - 79 publications, removed duplicates and 45 left
    - November 2019 - 1 new publication, duplicate and irrelevant
- Web of Science
    - January 2019 - 48 publications, removed duplicates and 44 left
    - November 2019 - 1 new publication, duplicate and irrelevant

The initial search performed during January 2019 returned 375 potentially relevant publications. Following duplicate removal, 326 publications remained and progressed to the title and abstract screening stage. Following screening for relevance based on title and abstract, 160 remained and entered the full text screening process. The full text articles for these publications were obtained for review. During the full text screening, process 11 publications were identified and obtained via a reverse reference search and added to the cohort of publications to be screened. Nine of these “reverse reference searched” publications remained following title and abstract screening. Thus, 169 publications entered the full text screening process. Seven full text articles could not be obtained, 3 were not available in English, 7 did not meet the inclusion criteria, 2 had duplicate results (same data in two publications) and 5 discussed ASFV isolation from ticks but not wild suids; hence these 24 publications were excluded from this scoping review.

A follow-up search was performed during November 2019 and returned 13 potentially relevant publications. Following duplicate removal and screening for relevance based on title and abstract, 0 publications remained.

One hundred and forty-five publications made up the final set of publications included in the scoping review. Figure 2 indicates the number of publications reviewed and excluded during each step of the review process (Moher *et al.*, 2009). It does not reflect the chronological order of events but rather the total number of publications included in each step of the review process. Despite including only 145 publications, some publications consisted of more than

one study type and some mentioned more than one virus or viral disease and some mentioned more than one animal species; hence the total reports of viral diseases in African ungulates for the different categories amounted to greater than 145.

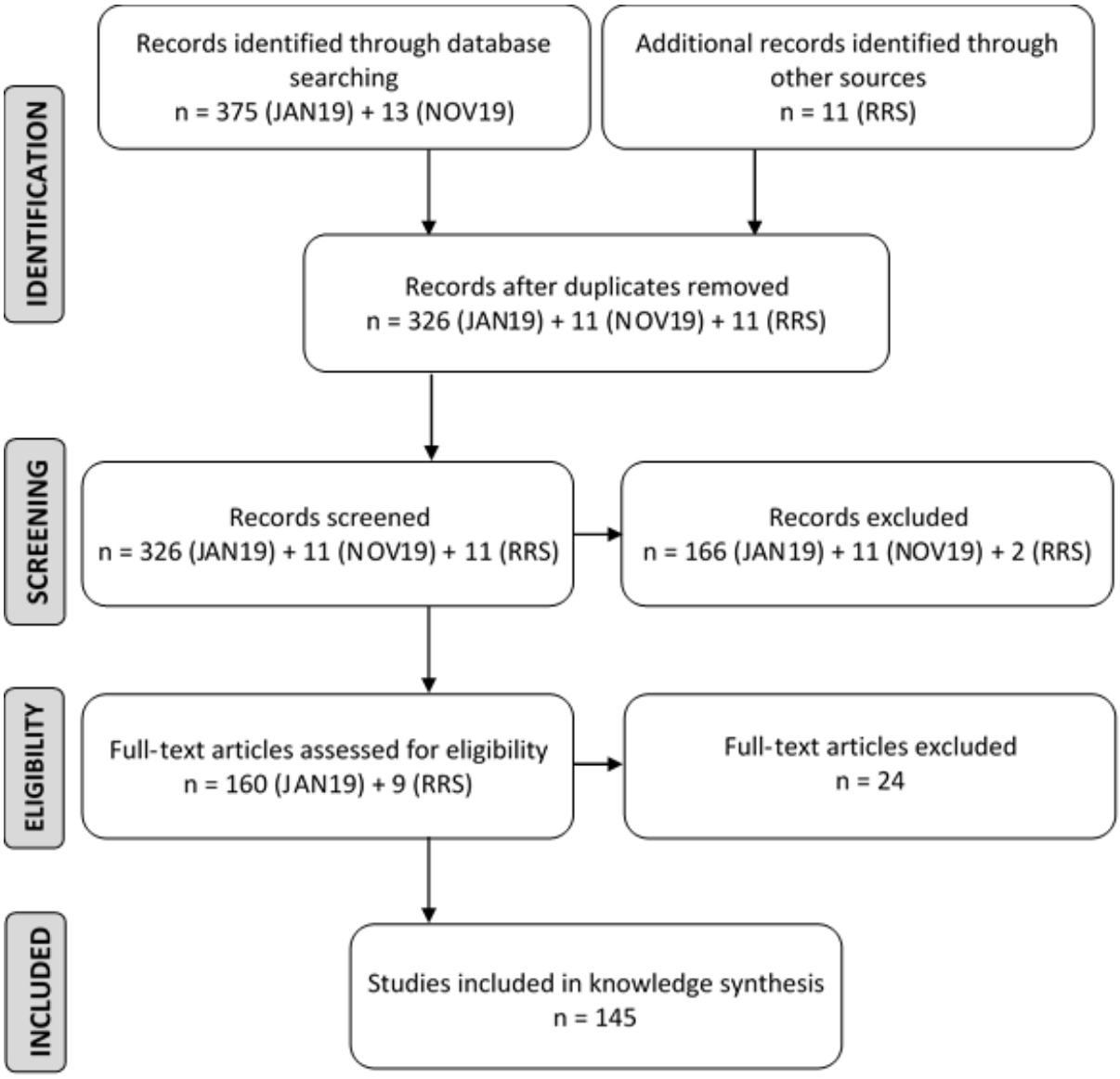


Figure 2: Flow diagram indicating the number of publications reviewed and excluded during each step of the review process, *RRS – Reverse Reference Search.

4.2. SYNTHESIS OF RESULTS

4.2.1. General characteristics of reported publications

Figure 3 summarises publications included in this study, by year of publication. The range of the publication dates were from 1957 to 2018. Sixteen percent of publications were published

in the last five years since January 2014 and 52% of studies were published between the start of 2000 and the end of 2018. The highest number of publications in a year was in 2015.

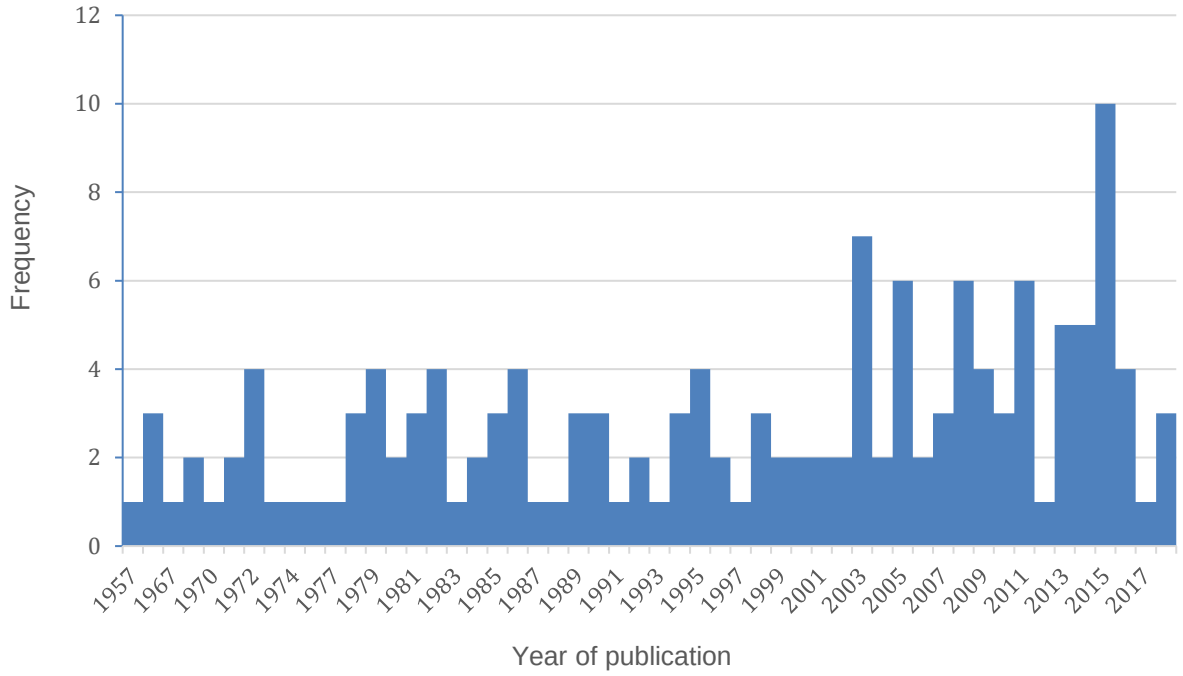


Figure 3: Number of publications reporting viral diseases in African ungulates per year from 1957 to 2018.

Most publications were surveillance studies, constituting 39% to the total publications (Table 1). The total number of publications in Table 1 was 148 even though the total number of publications were only 145. The reason for this discrepancy was that some publications contained more than one study type, for example both an experiment and surveillance study and counted more than once in the database. Furthermore, a large majority of the publications (95%) reported on viruses in free-ranging African ungulates and only 5% of publications reported on viruses in captive African ungulates.

Table 1: The proportion of different types of publications reporting on viruses/viral diseases in African ungulates.

Publication Type	Count of Publications	Percentage of total number of publications
Assay (molecular) development	1	1
Assay (antibody) development	4	3
Experiment	25	17
Phylogenetic study	29	20
Case/outbreak report	31	21
Surveillance	58	39
Total	**148**	

4.2.2. Viruses reported and diagnosed in African ungulates

A total of 32 viruses were reported by the 145 publications in African ungulates (Table 2). The five viruses with the most publications reporting on them in African ungulates, in descending order, were FMDV (27% of publications), ASFV (12% of publications), *alcelaphine gammaherpesvirus 1* (10% of publications), RVFP (5% of publications) and *elephantid betaherpesvirus 1/4/5* (5% of publications). The remaining 27 viruses only had 41% of publications report on them.

The total number for publications in Table 2 is 173 despite only 145 publications being included in this research study. The reason for this discrepancy is that some publications reported on more than one virus/viral disease in African ungulate species and counted more than once in the database.

Table 2: Number of publications reporting on each virus in African ungulates.

Virus	Publication count
Foot-and-mouth disease virus	46
African swine fever virus	20
Alcelaphine gammaherpesvirus 1	17
Rift Valley fever phlebovirus	9
Elephantid betaherpesvirus 1/4/5	8
Pestivirus A/B	7
Bluetongue virus	5
Bovine alphaherpesvirus 2	5
Rabies lyssavirus	5
Rinderpest morbillivirus	5
African horse sickness virus	4
Bovine alphaherpesvirus 1	4
Cardiovirus A	4
Equid alphaherpesvirus 1	4
Akabane orthobunyavirus	3
Bovine respirovirus 3	3
Lumpy skin disease virus	3
Bovine fever ephemerovirus	2
Bovine gammaherpesvirus 4	2
Deltapapillomavirus 4	2
Epizootic hemorrhagic disease virus	2
Equid alphaherpesvirus 9	2
Ovine gammaherpesvirus 2	2
African elephant polyomavirus 1	1
Alphaarterivirus equid	1
Bovine mastadenovirus	1

Equid alphaherpesvirus 4	1
Equine encephalosis virus	1
Hippotragine gammaherpesvirus 1	1
Pestivirus C	1
Small ruminant morbillivirus	1
Wesselsbron virus	1
Total	**173**

The number of reports that detected viral antigen/antibodies in African ungulates is shown in Table 3. FMDV was detected the most frequently in publications, accounting for 20% of the total reports of viruses detected. *Bovine alphaherpesvirus 2* accounted for 11% of the total reports of viruses detected. *Alcelaphine gammaherpesvirus 1* accounted for 9% of the total reports of viruses detected. *Pestivirus A/B* accounted for 7% of the total reports of viruses detected. BTV, *bovine alphaherpesvirus 1* and *bovine respirovirus 3* each accounted for 6% of the total reports of viruses detected. ASFV accounted for 5% of the total reports of viruses detected. RVFP accounted for 4% of the total reports of viruses detected. These nine viruses alone accounted for 74% of the total reports of viruses detected by antigen/antibody testing in African ungulates.

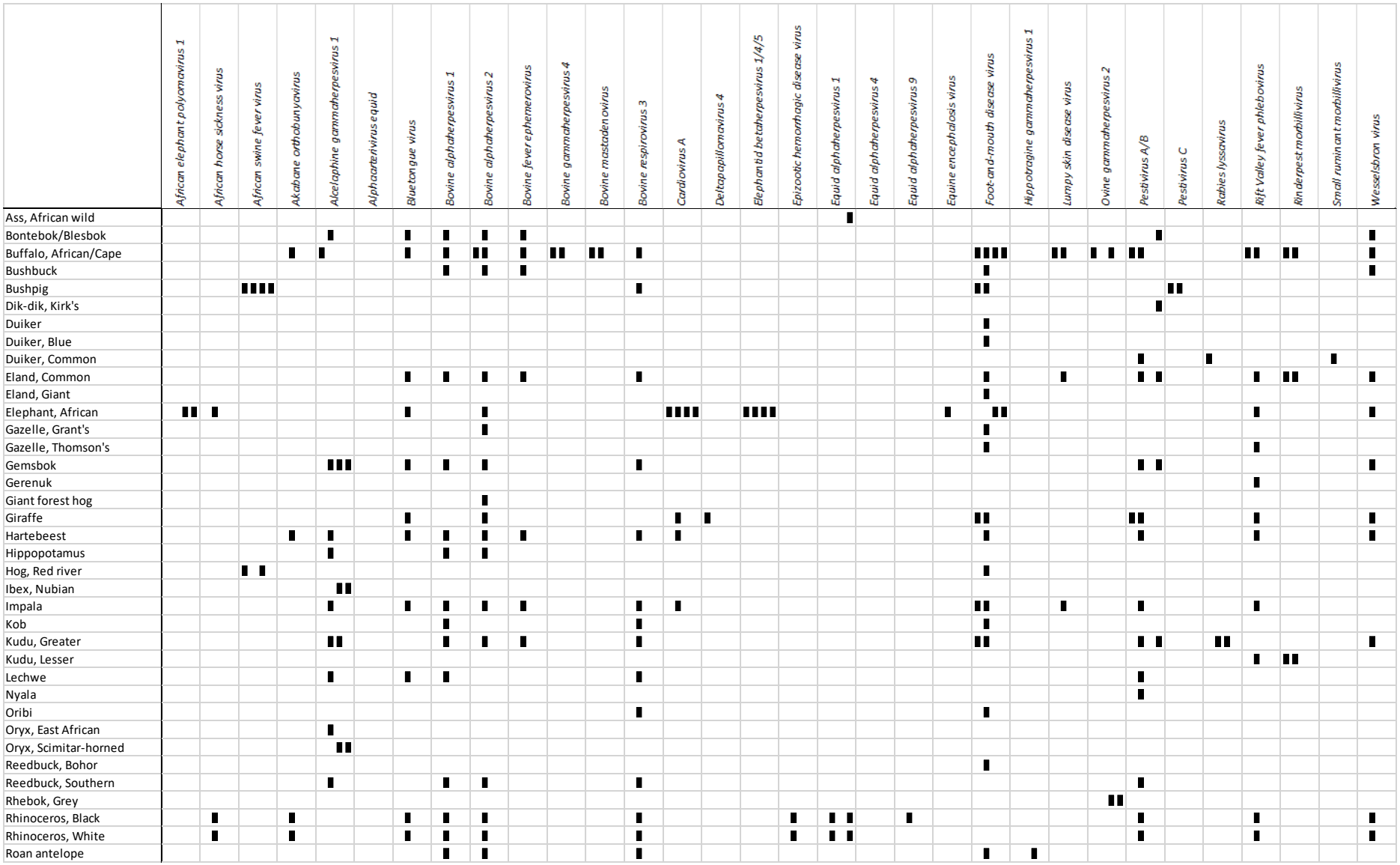
These reports were further classified according to the detection of viral antigen/antibody detected either in free-ranging or captive African ungulates (Figure 4). It is striking that *African elephant polyomavirus 1* has been detected only in captive animals according to published literature using antigen/antibody detection. The remainder of the viruses have either been diagnosed in a combination of free-ranging and captive animals, e.g. FMDV, ASFV, or only in free-ranging ungulates, e.g. *Akabane orthobunyavirus*, *bluetongue virus*.

Table 3: Number of publications indicating detection of viral antigen/antibody in each species of African ungulate.

	Total	*African horse sickness virus*	*Bluetongue virus*	*Epizootic hemorrhagic disease virus*	*Foot-and-mouth disease virus*	*Cardiovirus A*	*Small ruminant morbillivirus*	*Bovine respirovirus 3*	*Equid alphaherpesvirus 1*	*Equid alphaherpesvirus 9*	*Rinderpest morbillivirus*	*African swine fever virus*	*Bovine mastadenovirus*	*Alcelaphine gammaherpesvirus 1*	*Ovine gammaherpesvirus 2*	*Equine encephalosis virus*	*Rift Valley fever phlebovirus*	*Bovine alphaherpesvirus 1*	*Alphaarterivirus equid*	*Lumpy skin disease virus*	*Wesselsbron virus*	*Akabane orthobunyavirus*	*Bovine fever ephemerovirus*	*Pestivirus A/B*	*Equid alphaherpesvirus 4*	*Elephantid betaherpesvirus 1/4/5*	*Bovine gammaherpesvirus 4*	*Pestivirus C*	*Rabies lyssavirus*	*Hippotragine gammaherpesvirus 1*	*African elephant polyomavirus 1*	*Deltapapillomavirus 4*	*Bovine alphaherpesvirus 2*
Total	466	7	28	3	94	6	1	26	11	3	11	24	1	37	2	3	20	28	1	7	15	14	14	32	1	8	2	2	10	1	1	4	49
Ass, African wild	1								1																								
Bontebok/Blesbok	7		1											1				1			1		1	1									1
Buffalo, African/Cape	79		3		41			2			4		1	1	1		8	3		2	1	2	1	2			2						5
Bushbuck	8				1						1							1			1		1										3
Bushpig	9				1			1				6																1					
Dik-dik, Kirk's	1																							1									
Duiker	1				1																												
Duiker, Blue	1				1																												
Duiker, Common	3						1																	1					1				
Eland, Common	20		1		2			2			1						1	1		1	1		1	3					4				2
Eland, Giant	1				1																												
Elephant, African	20	2	1		1	3										1	1				1					8					1		1

Gazelle, Grant's	3				2																										1
Gazelle, Thomson's	3				2												1														
Gemsbok	13		2					2						3				1			1			2								2
Gerenuk	1																1														
Giant forest hog	1																														1
Giraffe	12		1		1	1				1							1				1			2						1	3
Hartebeest	18		3		3	1		1						2			1	1			1	1	1	1							2
Hippopotamus	4													1				1													2
Hog, Red river	3				1						2																				
Ibex, Nubian	1													1																	
Impala	29		3		14	1		1		1				1			1	1		1			1	1							3
Kob	3				1			1										1													
Kudu, Greater	22				5			1						2				2			1		1	3				5			2
Kudu, Lesser	3									2							1														
Lechwe	5		1					1						1				1						1							
Nyala	1																							1							
Oribi	2				1			1																							
Oryx, East African	2													1																	1
Oryx, Scimitar-horned	1													1																	
Reedbuck, Bohor	1				1																										
Reedbuck, Southern	5							1						1				1						1							1
Rhebok, Grey	1														1																
Rhinoceros, Black	14	1	1	1				1	2	1							1	1			1	2		1							1
Rhinoceros, White	16	1	2	2				1	2								1	2			1	2		1							1
Roan antelope	5				1			1										1										1			1
Sable antelope	8		1					1						2				1						1						1	1
Sheep, Barbary	1																							1							

Springbok	11		1					2											1	1	1	1	2										2
Tsessebe, Bangweulu	2		1										1																				
Tsessebe, Common/Topi	15		2		4			1					2				2				1	1											2
Warthog, Common	26				4			1				15				1					1		1				1						2
Warthog, Desert	1											1																					
Waterbuck	16		1		2			1					1				2				1	2	2										4
Wildebeest, Black	12		1					1					3				1		1	1	1	1	1										1
Wildebeest, Blue	34		2		3			2			1		12				3		1	1	1	2	2										4
Zebra, Grévy's	1								1																								
Zebra, Mountain	5	1							2						1																	1	
Zebra, Plains	14	2							3	2					1	1		1		1	1			1								1	



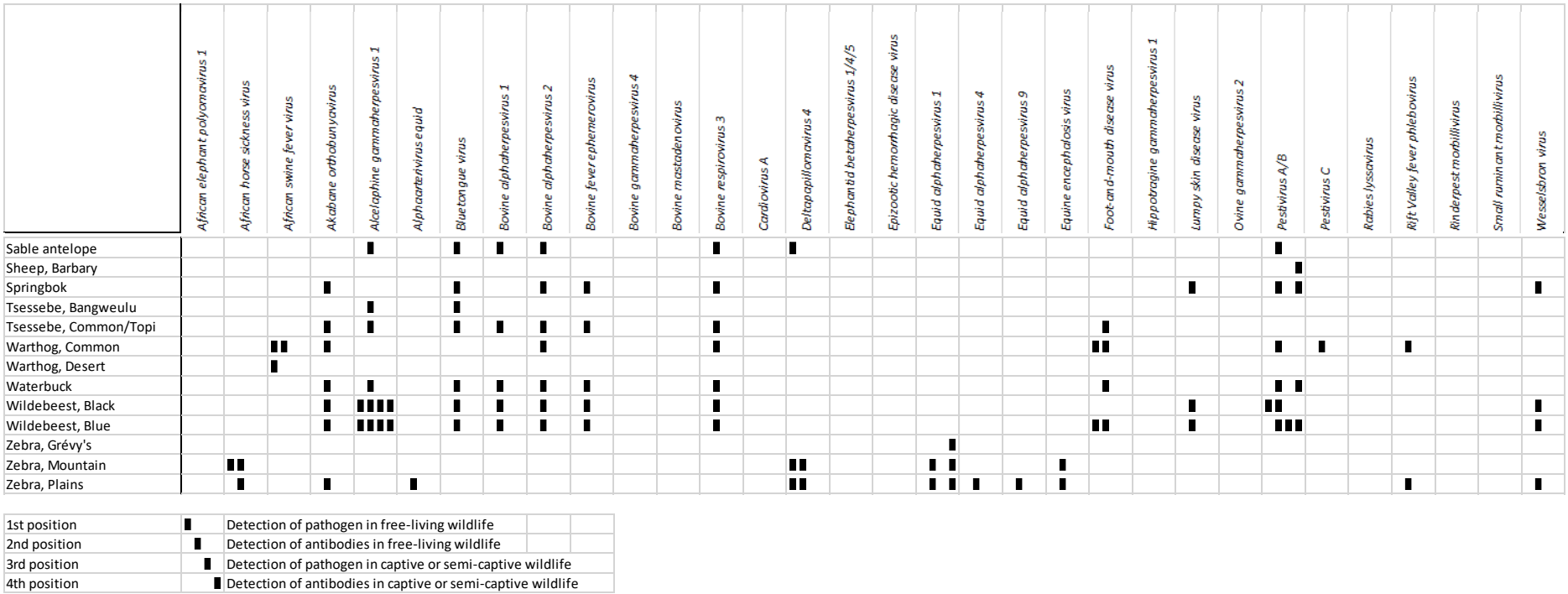


Figure 4: Detection of viral antigen/antibodies in free-living and semi-captive/captive African ungulates.

4.2.3. Specific ungulates affected by viruses

A wide variety of African ungulates were affected by viruses and a complete list is provided (Table 4). Of the 50 ungulate species affected by viruses the four African ungulates with the most viruses diagnosed via antigen/antibody detection, in descending order, were the African buffalo, blue wildebeest, impala and warthogs (common and desert). African buffalo accounted for 17% of antigen/antibody diagnosed viruses in African ungulates. This was by far the ungulate with the most reports. Blue wildebeest accounted for 7% of diagnosed viruses in African ungulates. Impala accounted for 6% of diagnosed viruses in African ungulates. Warthogs accounted for 6% of diagnosed viruses in African ungulates. The specific viruses with the most reports of being detected by antigen/antibody tests in specific ungulates were represented by 41 reports (8.8% of total reports) and 14 reports (3% of total reports) of FMDV in African buffalo and impala, respectively. There were 16 reports (3% of total reports) of ASFV in warthogs. There were also 12 reports (3% of total reports) of *alcelaphine gammaherpesvirus 1* in blue wildebeest.

Table 4: Number of publications reporting on virus detected in each African ungulate species.

Ungulate – common name	Ungulate – genus and species	Number of publications reporting virus detected
Ass, African wild	*Equus africanus*	1
Bontebok/Blesbok	*Damaliscus pygargus*	7
Buffalo, African/Cape	*Syncerus caffer*	79
Bushbuck	*Tragelaphus sylvaticus*	8
Bushpig	*Potamochoerus larvatus*	9
Dik-dik, Kirk's	*Madoqua kirkii*	1
Duiker	*Cephalophus silvicultor*	1
Duiker, Blue	*Philantomba monticola*	1
Duiker, Common	*Sylvicapra grimmia*	3
Eland, Common	*Taurotragus oryx*	20
Eland, Giant	*Taurotragus derbianus*	1
Elephant, African	*Loxodonta africana*	20
Gazelle, Grant's	*Gazella granti*	3
Gazelle, Thomson's	*Eudorcas thomsonii*	3
Gemsbok	*Oryx gazelle*	13
Gerenuk	*Litocranius walleri*	1
Giant forest hog	*Hylochoerus meinertzhageni*	1
Giraffe	*Giraffa camelopardalis*	12
Hartebeest	*Alcelaphus buselaphus*	18
Hippopotamus	*Hippopotamus amphibius*	4
Hog, Red river	*Potamochoeus porcus*	3

Ibex, Nubian	*Capra nubiana*	1
Impala	*Aepyceros melampus*	29
Kob	*Kobus kob*	3
Kudu, Greater	*Tragelaphus strepsiceros*	22
Kudu, Lesser	*Tragelaphus imberbis*	3
Lechwe	*Kobus leche*	5
Nyala	*Tragelaphus angasii*	1
Oribi	*Ourebia ourebi*	2
Oryx, East African	*Oryx beisa*	2
Oryx, Scimitar-horned	*Oryx dammah*	1
Reedbuck, Bohor	*Redunca redunca*	1
Reedbuck, Southern	*Redunca arundinum*	5
Rhebok, Grey	*Pelea capreolus*	1
Rhinoceros, Black	*Diceros bicornis*	14
Rhinoceros, White	*Ceratotherium simun*	16
Roan antelope	*Hippotragus equinus*	5
Sable antelope	*Hippotragus niger*	8
Sheep, Barbary	*Ammotragus lervia*	1
Springbok	*Antidorcas masupialis*	11
Tsessebe, Bangweulu	*Damaliscus superstes*	2
Tsessebe, Common/Topi	*Damaliscus lunatus*	15
Warthog, Common	*Phacochoerus africanus*	26
Warthog, Desert	*Phacochoerus aethiopicus*	1
Waterbuck	*Kobus ellipsiprymnus*	16
Wildebeest, Black	*Connochaetes gnou*	12
Wildebeest, Blue	*Connochaetes taurinus*	34
Zebra, Grévy's	*Equus grevyi*	1
Zebra, Mountain	*Equus zebra*	5
Zebra, Plains	*Equus quagga*	14
Grand Total		**466**

4.2.4. Geographical distribution of viruses

Of the 52 countries on the African continent, only 18 (35%) had viruses diagnosed in free-ranging ungulates, in the literature (Table 5).

Figure 5 provides a graphical depiction of the viruses reported in each country. Most reports of viruses originated from southern Africa (South Africa, Namibia, Botswana, Zimbabwe, Zambia, Eswatini and Mozambique) and east Africa (Tanzania, Kenya and Uganda) and a small proportion originated from north-, central- and west Africa. This confirms that all the publications in this study reported on viruses/viral diseases in ungulates from sub-Saharan Africa.

Table 5: Viruses diagnosed in ungulates per African country.

	African horse sickness virus	*African swine fever virus*	*Akabane orthobunyavirus*	*Alcelaphine gammaherpesvirus 1*	*Alphaarterivirus equid*	*Bluetongue virus*	*Bovine alphaherpesvirus 1*	*Bovine alphaherpesvirus 2*	*Bovine fever ephemerovirus*	*Bovine gammaherpesvirus 4*	*Bovine mastadenovirus*	*Bovine respirovirus 3*	*Cardiovirus A*	*Deltapapillomavirus 4*	*Elephantid betaherpesvirus 1/4/5*	*Epizootic hemorrhagic disease virus*	*Equid alphaherpesvirus 1*	*Equid alphaherpesvirus 4*	*Equid alphaherpesvirus 9*	*Equine encephalosis virus*	*Foot-and-mouth disease virus*	*Lumpy skin disease virus*	*Ovine gammaherpesvirus 2*	*Pestivirus A/B*	*Pestivirus C*	*Rabies lyssavirus*	*Rift Valley fever phlebovirus*	*Rinderpest morbillivirus*	*Small ruminant morbillivirus*	*Wesselsbron virus*	Total
BEN	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	**1**
BFA	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	**1**
BWA	0	1	0	0	0	1	1	1	0	0	0	1	0	0	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0	**12**
CAF	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	**1**
COD	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	**2**
GAB	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	**1**
KEN	1	6	1	3	0	1	1	2	0	2	0	1	0	0	1	1	0	0	0	0	3	1	0	1	0	0	3	4	0	0	**32**
MOZ	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	**1**
MWI	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	**2**
NAM	1	3	1	0	0	1	0	1	0	0	0	2	0	0	0	1	2	0	1	0	5	0	0	2	0	5	0	0	0	0	**25**
NGA	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	1	0	**5**
TCD	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	**3**
TZA	0	4	1	3	1	1	1	3	1	1	0	0	0	0	0	0	2	1	2	0	5	0	0	2	0	0	0	3	0	0	**31**
UGA	0	3	0	0	0	0	0	2	0	1	0	1	0	0	0	0	0	0	0	0	7	0	0	0	0	0	1	0	0	0	**15**

ZAF	3	6	2	7	0	3	2	2	1	1	0	3	2	2	2	2	2	0	0	1	22	2	1	2	1	1	7	0	0	1	**78**
ZMB	0	0	0	0	0	0	0	1	0	0	0	1	0	0	0	0	0	0	0	0	7	0	0	0	0	0	0	0	0	0	**9**
ZWE	0	3	0	0	0	0	0	1	0	0	1	1	0	0	0	0	0	0	0	0	14	0	0	0	0	0	0	0	0	0	**20**
Total	**5**	**30**	**5**	**13**	**1**	**7**	**5**	**14**	**2**	**5**	**1**	**11**	**2**	**2**	**3**	**4**	**6**	**1**	**3**	**1**	**80**	**3**	**1**	**7**	**1**	**6**	**11**	**7**	**1**	**1**	**239**

Country Abbreviation	Countries
BEN	Benin
BWA	Botswana
BFA	Burkina Faso
CAF	Central African Republic
TCD	Chad
COD	Democratic Republic of the Congo
SWZ	Eswatini
GAB	Gabon
KEN	Kenya
MWI	Malawi
MOZ	Mozambique
NAM	Namibia
NGA	Nigeria
NGA	Nigeria
NGA	Nigeria
ZAF	South Africa
TZA	Tanzania
UGA	Uganda
ZMB	Zambia
ZWE	Zimbabwe

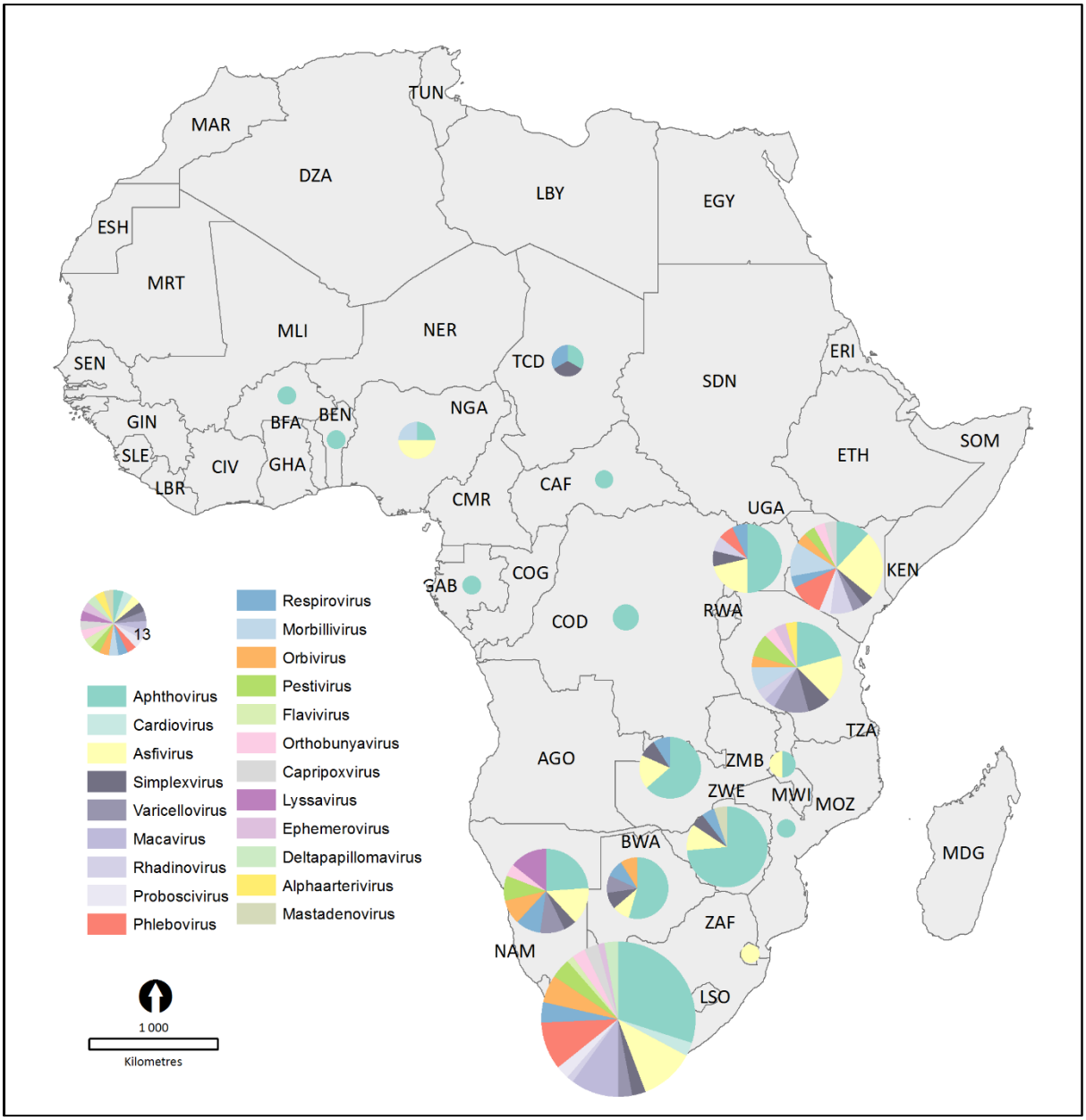


Figure 5: Geographical distribution of publications reporting on viruses in African ungulates.

4.2.5. Viruses which seem to be “under-studied”

Of the 32 viruses reported in African ungulates, several are classified as high-impact viruses. High-impact viruses have a significant negative impact on the health and lives of animals and humans due to their high morbidity/mortality rates in livestock, negative economic impacts and zoonotic potential (World Health Organization, 2014). A number of these viruses are also listed as notifiable diseases by the OIE (World Organisation for Animal Health, 2019).

The high-impact diseases which form part of the 32 reported diseases are:

- FMD
- ASF
- RVF
- Bluetongue
- Rabies
- LSD
- SRM
- AHS
- EHD
- Bovine viral diarrhea (BVD) (*Pestivirus A/B*)
- Bovine infectious bovine rhinotracheitis (IBR)/infectious pustular vulvovaginitis (IPV) (*Bovine alphaherpesvirus 1*)
- Equine influenza (*Influenza A virus*)
- Equine viral arteritis (*Alphaarterivirus equid*)
- Equine viral rhinopneumonitis (EHV1)
- CSF (*Pestivirus C*)

FMD, ASF, RVF, bluetongue and rabies are frequently reported on in the literature. On the contrary, LSD, PPR, AHS, EHD, BVD, bovine IBR/IPV, equine influenza, equine viral arteritis, equine viral rhinopneumonitis and CSF are infrequently reported on (Table 3).

A breakdown of the number of African ungulate species affected by a virus family/genus/species is provided (Table 6). The five virus species that affected the widest ranges of African ungulates are, in descending order: *bovine alphaherpesvirus 2* (24 of 50 ungulate species), FMDV (23 of 50 ungulate species), *Pestivirus A/B* (22 of 50 ungulate species), *bovine respirovirus 3* (21 of 50 ungulate species) and *bovine alphaherpesvirus 1* (20 of 50 ungulate species).

Table 6: The number of African ungulate species affected by a virus family/genus/ species.

Family	Count	Genus	Count	Species	Count
Adenoviridae	1	*Mastadenovirus*	1	*Bovine mastadenovirus*	1
Arteriviridae	1	*Alphaarterivirus*	1	*Alphaarterivirus equid*	1
Asfarviridae	4	*Asfivirus*	4	*African swine fever virus*	4
Flaviviridae	26	*Flavivirus*	15	*Wesselsbron virus*	15
		Pestivirus	23	*Pestivirus A/B*	22
				Pestivirus C	2
Herpesviridae	35	*Macavirus*	20	*Alcelaphine gammaherpesvirus 1*	18

				Ovine gammaherpesvirus 2	2
				Hippotragine gammaherpesvirus 1	1
		Proboscivirus	1	*Elephantid betaherpesvirus 1/4/5*	1
		Rhadinovirus	1	*Bovine gammaherpesvirus 4*	1
		Simplexvirus	24	*Bovine alphaherpesvirus 2*	24
		Varicellovirus	24	*Equid alphaherpesvirus 1*	6
				Equid alphaherpesvirus 9	2
				Bovine alphaherpesvirus 1	20
				Equid alphaherpesvirus 4	1
Papillomaviridae	4	*Deltapapillomavirus*	4	*Deltapapillomavirus 4*	4
Paramyxoviridae	25	*Morbillivirus*	7	*Small ruminant morbillivirus*	1
				Rinderpest morbillivirus	6
		Respirovirus	21	*Bovine respirovirus 3*	21
Peribunyaviridae	11	*Orthobunyavirus*	11	*Akabane orthobunyavirus*	11
Phenuiviridae	13	*Phlebovirus*	13	*Rift Valley fever phlebovirus*	13
Picornaviridae	23	*Aphthovirus*	23	*Foot-and-mouth disease virus*	23
		Cardiovirus	4	*Cardiovirus A*	4
Polyomaviridae	1	*Polyomavirus*	1	*African elephant polyomavirus 1*	1
Poxviridae	6	*Capripoxvirus*	6	*Lumpy skin disease virus*	6
Reoviridae	20	*Orbivirus*	20	*African horse sickness virus*	5
				Bluetongue virus	18
				Epizootic hemorrhagic disease virus	2
				Equine encephalosis virus	3
Rhabdoviridae	13	*Ephemerovirus*	12	*Bovine fever ephemerovirus*	12
		Lyssavirus	3	*Rabies lyssavirus*	3

5. DISCUSSION

5.1. SUMMARY OF EVIDENCE

This study provided a scoping review of published literature on viruses and their associated diseases in African ungulates. To our knowledge, it is the first of its kind on this topic, with the scientific community showing an increased interest in this area.

Several recommendations are outlined below for future research opportunities based on the general characteristics of reported publications, viruses reported and diagnosed in African ungulates, specific ungulates affected by viruses, the geographical distribution of viruses and viruses that seem to be “under-studied”. The intention of this scoping review was to provide a foundation for more focused analyses to be performed in future research projects. This will allow current knowledge to be built upon and new knowledge bases to be developed.

It has been established that many pathogens can infect and cause disease in both wildlife and livestock (Bengis *et al.*, 2004). However, wildlife health has only recently received attention, subsequent to research performed by Cleaveland *et al.* (2001) and Jones *et al.* (2008) who indicated that a large proportion of diseases emerging in human medicine originated from wildlife. In addition to this, it has been shown that the exposure of wildlife to domestic animals and/or human-generated activities, such as deforestation, urbanisation and agricultural intensification, play a major role as drivers for the emergence of wildlife diseases (Tompkins *et al.*, 2015).

The search for publications to be included in this study was constructed so that it would be comprehensive but still practical as well as making efficient use of human and time resources. Publications reporting cases of viral disease or detection of viral antigens/antibodies or molecular viral isolation in African ungulates were relevant to this study. The accuracy of the diagnosis made in the relevant publications broadly referring to viral disease in African ungulates were beyond the scope of this research study.

A number of publications were not detected during the search process by interrogating the database using the search string and were found via a reverse reference search process. The reason for publications not being detected during the search process would most likely be due to the manner in which the databases’ search algorithms work. For example, the publications not initially detected may not have had specific words in their titles, abstracts or keyword lists or the correct combination of words between the three categories for the database algorithm to include the publications in the search results.

5.1.1. General characteristics of reported publications

Results show that about half of the publications that focused on viral diseases in African ungulates occurred during the last 8 years. This confirmed that there is an increasing interest in this field amongst scientists. Only 21% of the publications were case reports, indicating that case reports of viral disease in African ungulates are under-studied or under-published. Furthermore, a large majority of the publications discussed viruses in free-ranging African ungulates and only 5% of the publications discussed viruses in captive African ungulates. This is interesting as it would be expected that it would be easier to obtain samples from captive animals; however, the population sizes of captive African ungulates are small in comparison to their free-ranging counterparts and prior to animals becoming captive they are likely to undergo testing for certain diseases. If they provide a positive result, they are unlikely to be placed into a captive collection.

5.1.2. Viruses reported and diagnosed in African ungulates

The viruses of significance, according to the number of publications that have reported on them are FMDV, ASFV, *alcelaphine gammaherpesvirus 1* and RVFP (Table 3). These four viruses account for more than 50% of the published research and reports on viral diseases in African ungulates. Based on the number of reports of viral antibody/antigen detected in African ungulates FMDV, *bovine alphaherpesvirus 2*, *alcelaphine gammaherpesvirus 1*, *Pestivirus A/B*, BTV, *bovine alphaherpesvirus 1*, *bovine respirovirus 3*, ASFV and RVFP featured amongst the viruses most detected in African ungulates (Figure 4). This is likely because several of the publications involved viral antigen/antibody surveillance of large numbers of wild African ungulates.

FMD and ASF are two of the diseases of high interest due to their economic importance but neither are zoonotic (Penrith *et al.*, 2019a, Thomson and Bastos, 2004). Zoonotic viral diseases, such as RVF and rabies are of high importance because of the disease they cause in humans (Markotter *et al.*, 2018, Swanepoel and Coetzer, 2004). These diseases of high interest generally stimulate public and political interest and will automatically attract funding for research. In comparison, some viral diseases exclusive to animals which are listed as being diseases of high impact, e.g., AHS and SRM, have significantly less research associated with them, likely due to the fact that they are of low economic, political and zoonotic interest within the context of African wildlife (Coetzer and Guthrie, 2004, Rossiter, 2004). In addition, most of the other diseases which have high numbers of reports of being detected by antigen/antibody testing in African ungulates do not cause serious clinical disease in free-ranging wildlife, at

least not that has been documented (Machlachlan and Savini, 2018, O'Toole and Li, 2018, Penrith *et al.*, 2019a, Swanepoel and Coetzer, 2004).

FMDV has the largest number of publications reporting on it and has been detected the most by antigen/antibody testing in African ungulates compared to the other 31 viruses (Table 3 and Figure 4). Despite being significant, based on research and its impact on the global economy, it is a virus which does not cause clinically significant disease in free-ranging African ungulates (Thomson and Bastos, 2004). It will only on occasion, specifically when the animals are stressed, cause significant morbidity - for example, when animals are held in a *boma* facility for research purposes or relocation. A likely reason for FMD receiving so much attention is that it is a highly trade sensitive disease. This reflects that funding into disease research is often driven by economic and political agendas (Thomson and Bastos, 2004, Weaver *et al.*, 2013). In contrast, a virus such as rabies has a significantly smaller number of publications reporting on it in African ungulates despite causing widespread mortality and significant clinical disease, even in ungulates, and it is a serious zoonotic risk (Hassel *et al.*, 2018, Markotter *et al.*, 2018, Scott *et al.*, 2012).

In the case of ASF, years of funding and research have provided very limited effectiveness in reducing outbreaks of the disease and, at time the of writing, there were two major outbreaks occurring across Europe and Asia, driven by increased and easier global travel, trade in pork (legal and illegal) and poor biosecurity measures, e.g. feeding of animal products to animals (Penrith *et al.*, 2019b). Recently, there has been a change in research focus from wild suids to argasid ticks and socioeconomic factors that drive the spread of ASF. This indicates that scientists are realising that these are the key issues requiring attention rather than wild suids being the reservoir of ASF. For most viruses, the impacts of infection, whether they cause clinical or subclinical infection in African ungulates, is limited (Kock, 2014). Transmission of ASF to domestic pigs at the wildlife/livestock interface in Africa is often suggested but a true interface is rarely documented (Penrith *et al.*, 2019b). The spread of ASF to Europe and Asia, and throughout, is driven by trade in pork and poor biosecurity measures with minimal involvement of wild suids (Penrith *et al.*, 2019b).

Alcelaphine gammaherpesvirus 1, causing MCF, featured high up on the list of viruses when it came to the number of publications reporting on it and reports of its detection by antigen/antibody testing in African ungulates (Table 3 and Figure 4). This is interesting because to date, very few clinical cases of MCF have been reported in free-ranging African ungulates and a few cases have been reported in captive African buffalo (Pfitzer *et al.*, 2015). The reason for this finding is most likely due to the fact that MCF is readily transmitted from blue and black wildebeest to cattle in conditions where they live in close proximity to each

other (Hussain *et al.*, 2017, Pfitzer *et al.*, 2015). This confirms that certain viruses are not of great significance in African wildlife but are of significance to livestock producers and hence will receive funding and interest from the agricultural sector. In addition, given the only free-ranging African ungulate in which clinical disease of MCF has been reported is the African buffalo, it is recommended that MCF surveillance and research take place in buffalo in the future as it may be an emerging viral disease in this species (Pfitzer *et al.*, 2015).

RVFP is a significant virus in the context of human, livestock and wildlife health, hence it deserves to be listed as one of the viruses which had a high number of publications reporting on it and had a large number of reports of being detected by antigen/antibody testing in African ungulates (Table 3 and Figure 4). As an example, in 2010 there was an outbreak of RVF in South Africa, with the first case being reported in January 2010 in the Free State province. By the end of the outbreak, the disease had been reported in eight of the nine provinces, KwaZulu Natal being the only unaffected province (Métras *et al.*, 2013, Pienaar and Thompson, 2013). It was also the first time in the history of RVF outbreaks in South Africa that a winter rainfall area, i.e. the Western Cape, was affected (Pienaar and Thompson, 2013). The government reported 237 confirmed human cases of RVF with 26 deaths and large numbers of animals, including sheep, goats, cattle and wildlife, were affected (Pienaar and Thompson, 2013, World Health Organization, 2010). Based on this outbreak, RVFP is evidently a pathogen of animal origin that has extended its host range and is able to infect humans. The outbreak seemed to be driven by climatic and ecological changes, resulting in increased rainfall, as well as anthropogenic ecological changes (man-made dams and agricultural intensification) resulting in increased populations of mosquitoes. Despite ongoing research and the availability of vaccinations, this zoonotic disease, endemic to Africa's tropical regions, is of significance as it has the potential to become a global emerging disease if a One Health management strategy is not implemented to manage it (Beechler *et al.*, 2015, Fagbo *et al.*, 2014).

A noteworthy observation is that FMDV, *bovine alphaherpesvirus 2*, *alcelaphine gammaherpesvirus 1*, *Pestivirus A/B*, BTV, *bovine alphaherpesvirus 1*, *bovine respirovirus 3*, ASFV and RVFP are all viruses of great significance in domestic livestock agriculture, hence the reason for their surveillance in wildlife, but only a few of them cause significant clinical disease in free-ranging African ungulates. Additionally, there was some overlap, but also some discrepancy between the number of publications reporting on viruses and the reports of viral antigen/antibody detected in African ungulates, i.e. ASFV and RVFP were lower down on the ranking of viruses reported to be detected by antigen/antibody testing in African ungulates compared to a high ranking of viruses reported on by number of publications. A possible reason for this discrepancy with ASFV may be that ASFV is very hard to detect in wild suids and a large number of publications focused on its detection in argasid ticks, which were

outside the scope of this research study. Surveillance of ASFV in wild suids is very limited resulting in a low ranking of viruses detected by viral antibody/antigen detection. In the case of RVFP, the virus has a narrow region of infection, generally tropical areas with high rainfall, and has recently become an emerging disease and spread to new geographical areas. Surveillance for RVFP has not been as significant as for some of the older viruses, ranking low on viruses detected by viral antibody/antigen detection. There has only recently been a greater research focus on this virus.

African elephant polyomavirus 1 is the only virus that was solely diagnosed in captive animals according to published literature using antigen/antibody detection (Figure 4). This is possibly because this is a new virus, diagnosed 7 years ago, and there has not been much research investigating it (Stevens *et al.*, 2013). The remainder of the viruses, Figure 4, have either been diagnosed in a combination of free-ranging and captive animals, e.g. FMDV, ASFV, or only in free-ranging ungulates, e.g. *Akabane orthobunyavirus*, *bluetongue virus*. It appeared that viruses that were diagnosed in both free-ranging and captive animals, e.g. FMDV, ASFV, were the viruses that seemed to have the most publications reporting on them, likely because these viruses were the ones of major interest in the wildlife and livestock agricultural sectors. It is recommended that future research in this field be focused on *African elephant polyomavirus 1*. However, currently the virus does not seem to bear severe consequences or risks for the health of free-ranging elephants, therefore passive or low-grade active surveillance can be performed in addition to other diseases being researched/surveyed to maximise resource use. An additional recommendation is to perform research dedicated to investigating *Akabane orthobunyavirus* and its relationship with black and white rhinoceros as it may be of interest to the conservation of these endangered species.

5.1.3. Specific ungulates affected by viruses

A wide variety of African ungulates are affected by viruses as listed in Table 4.

Seventeen percent of diagnosed viruses/viral diseases in African ungulates were represented by the African buffalo, which was by far the ungulate diagnosed with the most viruses. African buffalo are susceptible to 16 of the 32 viruses mentioned in this study. This may be because African buffalo are widely spread across sub-Saharan Africa, they are one of the most studied wild African ungulates due to their association with FMD and possibly because they are reasonably easy to locate, immobilise and sample.

Blue wildebeest represented 7% of diagnosed viruses/viral diseases in African ungulates with a high number of publications reporting on *alcelaphine gammaherpesvirus 1*. This indicates the relationship between the blue wildebeest and *alcelaphine gammaherpesvirus 1*, with blue

wildebeest being the reservoir host for this virus (O'Toole and Li, 2018). Blue wildebeest are also an ungulate species very commonly found throughout sub-Saharan Africa.

Impala represented 6% of diagnosed viruses/viral diseases in African ungulates. Once again this may be because FMD was the viral disease which had the most publications reporting on it. Impala are also widely spread across sub-Saharan Africa.

Warthogs also represented 6% of diagnosed viruses/viral diseases in African ungulates. This may be because the warthog is the wild reservoir host for ASFV and ASF was the viral disease with the second highest number of publications reported (Penrith *et al.*, 2019a). Warthogs also inhabit vast areas of sub-Saharan Africa.

5.1.4. Geographical distribution of viruses

All the publications in this study reported on viruses/viral diseases in ungulates from sub-Saharan Africa. The geographical distribution map indicates that the majority of the publications reported on viruses/viral diseases in ungulates in southern and eastern Africa, with a small proportion from western Africa and none from central or northern Africa. Several factors may contribute to this distribution. The most likely factor would be the concentration of research institutions and funding available in each of these geographical regions of Africa, with higher concentrations present in more developed African countries. Another factor could be past or ongoing war and conflict. Countries severely affected by war have lower numbers of publications, given wildlife numbers are decimated during war and scientists are less likely to work in countries where their lives are in danger (Bliziotis *et al.*, 2005, Wiethoelter *et al.*, 2015). Examples of countries affected by war include Angola and Mozambique. There were 0 publications reporting on viruses/viral diseases in ungulates from Angola and only 1 from Mozambique, despite both countries being in southern Africa. Furthermore, several studies originated from continents besides Africa, namely Europe and North America. These studies were included for thoroughness and pertain to viral diseases in wild African ungulates in captivity, but their data was not used to calculate percentages of publications dealing with free-range compared to captive ungulates.

5.1.5. Viruses which seem to be “under-studied”

Of the 32 viruses reported to infect African ungulates, several are classified as high-impact viruses because they have a significant negative impact on the health and lives of animals and humans (World Health Organization, 2014) and are listed as notifiable diseases to the OIE (World Organisation for Animal Health, 2019). The high-impact viral diseases diagnosed in African ungulates that are of significance in the African context are as follows:

- FMD
- ASF
- RVF
- Bluetongue
- Rabies
- LSD
- SRM
- AHS

Interestingly, a virus species that affects a wide range of African ungulates does not necessarily classify that particular virus as high-impact. For example, of the top five virus species affecting the widest ranges of African ungulates; FMDV, *Pestivirus A/B* and *bovine alphaherpesvirus 1* form part of the high-impact viruses and only FMDV is of significance in the African context.

Certain diseases, such as SRM, which can have a significant impact on wildlife, do not seem to receive as much attention as they could have. It may be necessary to add a new "wildlife" category to the OIE-listed diseases. This is an important consideration, especially to allow future conservation efforts and campaigns to take diseases into account, as infectious diseases are becoming more prevalent in wildlife populations with the intensification of agriculture and the increased amount of wildlife/livestock/human interactions (Cunningham *et al.*, 2017). The OIE-listed diseases pertain to the World Trade Organisation, if certain diseases are threatening the conservation and/or associated economy of a wildlife species, then ideally trade that may spread that disease should be halted.

A clear knowledge gap is highlighted in research focusing on LSDV, SRM and AHSV. The reason for the under reporting of research on some diseases may be due to the difficulty of surveillance for disease in free-ranging African ungulates. For example, game rangers may come across a dead animal and if the carcass is fresh, samples may be collected. However, synthesising a case report from limited information is particularly challenging and unlikely to be published in a peer-reviewed scientific journal unless it is of great significance. Another reason these diseases may be under-reported is that LSD and AHS do not cause significant clinical disease in African ungulates. In addition, disease research focuses mainly on livestock, instead of wildlife, because agriculture and food production play a major role in the economies of countries across the globe. Therefore, many publications discussing diseases in wildlife is due to the disease being important in livestock. A good example of this is FMD that is a very important disease in livestock but much less so in wildlife. Nevertheless, these diseases are of great significance in the context of livestock health and given African ungulates may play a

role in the epidemiology of these diseases, it is important that these diseases are strongly considered as research topics in the future.

5.2. LIMITATIONS AND CONSTRAINTS

This research study has several limitations. In the first instance, it was predisposed to database bias as only three multidisciplinary databases were interrogated during the search process and the search strategy delivered mainly veterinary related articles. If other databases were interrogated additional publications may have been obtained (Pham *et al.* 2014). Given this scoping review was based on scientific publications, it was predisposed to publication bias affected by author's career status, institution, language, country, study outcome, research topic, research sponsor and timeline (Song *et al.*, 2010, Song *et al.*, 2013). This study was also prone to spatial bias as research and publication concentrate in more developed countries, e.g., Zimbabwe (prior to 1985), South Africa, Namibia, Botswana, Kenya and Tanzania, due to being correlated to economic indices (Bliziotis *et al.*, 2005). Geographical bias also plays a role, as there was an underrepresentation of publications from specific regions in Africa, in particular north-, west- and central Africa, and may suggest limited resources and capacity for wildlife surveillance in these areas.

Constraints were necessary and were put into place to maintain a practicable scope for this research study. The importance of viral diseases in terms of economic, health and conservation impacts were not quantified. Only viral diseases diagnosed in African ungulates were relevant and deemed sufficiently extensive to satisfy the objectives of the scoping review. All indigenous African ungulates were listed and included in the search. This may have resulted in the exclusion of a very rare ungulate species that may not have been identified yet but this scenario is highly unlikely.

Categorising wildlife into captive, semi-captive and free-ranging could not be achieved during the search process, given the constraints of the methodology. Hence, only two categories, namely captive and free-ranging wildlife, were set.

Given the limitations of this research study, it is necessary to highlight that the findings presented in this discussion indicate the perceived emphasis placed on different viruses and viral diseases by scientists and should not be perceived as the incidence or occurrence of viral diseases in African ungulates. In fact, a sound knowledge of the ecosystem dynamics for many multi-host viral diseases is deficient (Roche and Guegan, 2011). Therefore, it would be recommended that research is performed in this field, including quantitative research focusing on viral diseases in African ungulates, to further clarify the role of wildlife in the epidemiology

of these diseases, and, moreover, to provide evidence of the importance of these diseases at the wildlife/livestock interface.

5.3. CONCLUSION

The viral diseases of African ungulates which have received the most attention over the past six decades have been highlighted, as well as which diseases have not received the attention they could have. There are a variety of viruses which have been diagnosed in African ungulates and all African ungulates identified have had one or more viruses or viral diseases associated with them.

It is anticipated that these findings will be valuable to policymakers, funding bodies, researchers and other stakeholders who need an understanding of viral diseases in African ungulates. Research opportunities in this field will allow them to make informed decisions about investment in future research projects and animal health policies and protocols. It is recommended that governments and research institutions offer more funding to investigate and report viral diseases of greater clinical and zoonotic significance, such as rabies and Rift Valley fever. This is especially important in the current climate of emerging diseases and the related overflow of disease from wild to domestic animals and from animals, both wild and domestic, to humans. A further recommendation is for appropriate One Health approaches to be adopted for investigating, controlling, managing and preventing diseases (Cunningham *et al.*, 2017). This is especially true for diseases such as African swine fever and Rift Valley fever where human actions, poor biosecurity and natural weather changes play a major role in the transmission of diseases (Cunningham *et al.*, 2017, Penrith *et al.*, 2019a, Swanepoel and Coetzer, 2004). Diseases which may threaten the conservation of certain wildlife species also require focused attention. In order to keep track of these diseases it may be necessary to consider adding a “wildlife” category to the OIE-listed diseases.

Viral diseases, as a whole, are of great significance and require extra attention in the future as they make up a large proportion of emerging infectious diseases and can often infect multiple hosts (Bengis *et al.*, 2004, Cleaveland *et al.*, 2001). Hence, the viruses and viral diseases diagnosed in African ungulates are of significance, particularly at the wildlife/livestock interface and many of them have the potential of becoming emerging wildlife diseases.

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8. Appendix A: Preferred reporting items for systematic reviews and meta-analyses extension for scoping reviews (PRISMA-ScR) checklist

SECTION	ITEM	PRISMA-ScR CHECKLIST ITEM	REPORTED ON PAGE #
TITLE			
Title	1	Identify the report as a scoping review.	Cover page
ABSTRACT			
Structured summary	2	Provide a structured summary that includes (as applicable): background, objectives, eligibility criteria, sources of evidence, charting methods, results, and conclusions that relate to the review questions and objectives.	1
INTRODUCTION			
Rationale	3	Describe the rationale for the review in the context of what is already known. Explain why the review questions/objectives lend themselves to a scoping review approach.	4
Objectives	4	Provide an explicit statement of the questions and objectives being addressed with reference to their key elements (e.g., population or participants, concepts, and context) or other relevant key elements used to conceptualize the review questions and/or objectives.	5
METHODS			
Protocol and registration	5	Indicate whether a review protocol exists; state if and where it can be accessed (e.g., a Web address); and if available, provide registration information, including the registration number.	17
Eligibility criteria	6	Specify characteristics of the sources of evidence used as eligibility criteria (e.g., years considered, language, and publication status), and provide a rationale.	17
Information sources*	7	Describe all information sources in the search (e.g., databases with dates of coverage and contact with authors to identify additional sources), as well as the date the most recent search was executed.	17
Search	8	Present the full electronic search strategy for at least 1 database, including any limits used, such that it could be repeated.	17
Selection of sources of evidence†	9	State the process for selecting sources of evidence (i.e., screening and eligibility) included in the scoping review.	19
Data charting process‡	10	Describe the methods of charting data from the included sources of evidence (e.g., calibrated forms or forms that have been tested by the team before their use, and whether data charting was done	20

SECTION	ITEM	PRISMA-ScR CHECKLIST ITEM	REPORTED ON PAGE #
		independently or in duplicate) and any processes for obtaining and confirming data from investigators.	
Data items	11	List and define all variables for which data were sought and any assumptions and simplifications made.	20
Critical appraisal of individual sources of evidence§	12	If done, provide a rationale for conducting a critical appraisal of included sources of evidence; describe the methods used and how this information was used in any data synthesis (if appropriate).	22
Synthesis of results	13	Describe the methods of handling and summarizing the data that were charted.	22
RESULTS			
Selection of sources of evidence	14	Give numbers of sources of evidence screened, assessed for eligibility, and included in the review, with reasons for exclusions at each stage, ideally using a flow diagram.	23
Characteristics of sources of evidence	15	For each source of evidence, present characteristics for which data were charted and provide the citations.	24
Critical appraisal within sources of evidence	16	If done, present data on critical appraisal of included sources of evidence (see item 12).	N/A
Results of individual sources of evidence	17	For each included source of evidence, present the relevant data that were charted that relate to the review questions and objectives.	N/A
Synthesis of results	18	Summarize and/or present the charting results as they relate to the review questions and objectives.	24
DISCUSSION			
Summary of evidence	19	Summarize the main results (including an overview of concepts, themes, and types of evidence available), link to the review questions and objectives, and consider the relevance to key groups.	40
Limitations	20	Discuss the limitations of the scoping review process.	47
Conclusions	21	Provide a general interpretation of the results with respect to the review questions and objectives, as well as potential implications and/or next steps.	48
FUNDING			
Funding	22	Describe sources of funding for the included sources of evidence, as well as sources of funding for the scoping review. Describe the role of the funders of the scoping review.	49

JBI = Joanna Briggs Institute; PRISMA-ScR = Preferred Reporting Items for Systematic reviews and Meta-Analyses extension for Scoping Reviews.

* Where *sources of evidence* (see second footnote) are compiled from, such as bibliographic databases, social media platforms, and Web sites.

† A more inclusive/heterogeneous term used to account for the different types of evidence or data sources (e.g., quantitative and/or qualitative research, expert opinion, and policy documents) that may be eligible in a scoping review as opposed to only studies. This is not to be confused with *information sources* (see first footnote).

‡ The frameworks by Arksey and O'Malley (6) and Levac and colleagues (7) and the JBI guidance (4, 5) refer to the process of data extraction in a scoping review as data charting.

§ The process of systematically examining research evidence to assess its validity, results, and relevance before using it to inform a decision. This term is used for items 12 and 19 instead of "risk of bias" (which is more applicable to systematic reviews of interventions) to include and acknowledge the various sources of evidence that may be used in a scoping review (e.g., quantitative and/or qualitative research, expert opinion, and policy document).

From: Tricco AC, Lillie E, Zarin W, O'Brien KK, Colquhoun H, Levac D, *et al.* PRISMA Extension for Scoping Reviews (PRISMA-ScR): Checklist and Explanation. Ann Intern Med.;169:467–473. doi: 10.7326/M18-0850

9. Appendix B: Search strings

9.1. General search string

Africa* AND (virus OR viral) AND (loxodonta OR “african elephant” OR giraff* OR syncerus OR “african buffalo” OR “cape buffalo” OR hippopotamus OR choeropsis OR rhinoceros OR ceratotherium OR diceros OR “equus zebra” OR “equus africanus” OR grevyi OR quagga OR phacochoerus OR warthog OR potamochoerus OR bushpig OR “red river hog” OR aepyceros OR impala OR alcelaphus OR hartebees* OR connochaetes OR wildebees* OR damaliscus OR tsessebe OR bonteb* OR blesb* OR antidorcas OR springb* OR raphicerus OR steenb* OR grysbok OR tragelaphus OR kudu OR koedoe OR nyala OR bongo OR bushbuck OR bosbok OR sitatunga OR taurotragus OR eland OR hippotragus OR sable OR roan OR oryx OR gemsb* OR pelea OR rheb* OR redunca OR reedbuck OR rietbok OR “kobus ellipsiprymnus” OR waterb* OR “kobus leche” OR lechwe OR “kobus kob” OR “kobus vardonii” OR puku OR cephalophus OR sylvicapra OR philantomba OR duiker OR oreotragus OR klipspringer OR spekei OR leptoceros OR "Gazella dorcas" OR eudorcas OR nanger OR addax OR “capra nubiana” OR “nubian ibex” OR beatragus OR hirola OR ammotragus OR "barbary sheep" OR dorcatragus OR madoqua OR "dik-dik" OR okapia OR okapi OR neotragus OR "royal antelope" OR suni OR litocranius OR gerenuk OR hyemoschus OR chevrotain OR ourebia OR oribi) AND NOT (beetle OR arthropod OR oryctes OR nudivirus OR javan OR sumatran OR “one horned” OR snake OR chicken* OR human* OR Newcastle OR arabian OR tragus OR aquaculture OR waterborne)

9.2. Adapted for Scopus

(TITLE-ABS-KEY (africa*) AND TITLE-ABS-KEY (virus OR viral)) AND (TITLE-ABS-KEY (loxodonta OR "african elephant" OR giraff* OR syncerus OR "african buffalo" OR "cape buffalo" OR hippopotamus OR choeropsis OR rhinoceros OR ceratotherium OR diceros OR "equus zebra" OR "equus africanus" OR grevyi OR quagga OR phacochoerus OR warthog OR potamochoerus OR bushpig OR "red river hog" OR aepyceros OR impala OR alcelaphus OR hartebees* OR connochaetes OR wildebees* OR damaliscus OR tsessebe OR bonteb* OR blesb* OR antidorcas OR springb* OR raphicerus OR steenb* OR grysbok OR tragelaphus OR kudu OR koedoe OR nyala OR bongo OR bushbuck OR bosbok OR sitatunga OR taurotragus OR eland OR hippotragus OR sable OR roan OR oryx OR gemsb* OR pelea OR rheb* OR redunca OR reedbuck OR rietbok OR "kobus ellipsiprymnus" OR waterb* OR "kobus leche" OR lechwe OR "kobus kob" OR "kobus vardonii" OR puku OR cephalophus OR

sylvicapra OR philantomba OR duiker OR oreotragus OR klipspringer OR spekei OR leptoceros OR "Gazella dorcas" OR eudorcas OR nanger OR addax OR "capra nubiana" OR "nubian ibex" OR beatragus OR hirola OR ammotragus OR "barbary sheep" OR dorcatragus OR madoqua OR "dik-dik" OR okapia OR okapi OR neotragus OR "royal antelope" OR suni OR litocranius OR gerenuk OR hyemoschus OR chevrotain OR ourebia OR oribi)) AND NOT (TITLE-ABS-KEY (beetle OR arthropod OR oryctes OR nudivirus OR javan OR sumatran OR "one horned" OR snake OR chicken* OR human* OR Newcastle OR arabi* OR tragus OR aquaculture OR waterborne))

9.3. Adapted for Wildlife & Ecology Studies Worldwide

TI (Africa*) AND TI (virus OR viral) AND TI (loxodonta OR "african elephant" OR giraff* OR syncerus OR "african buffalo" OR "cape buffalo" OR hippopotamus OR choeropsis OR rhinoceros OR ceratotherium OR diceros OR "equus zebra" OR "equus africanus" OR grevyi OR quagga OR phacochoerus OR warthog OR potamochoerus OR bushpig OR "red river hog" OR aepyceros OR impala OR alcelaphus OR hartebees* OR connochaetes OR wildebees* OR damaliscus OR tsessebe OR bonteb* OR blesb* OR antidorcas OR springb* OR raphicerus OR steenb* OR grysbok OR tragelaphus OR kudu OR koedoe OR nyala OR bongo OR bushbuck OR bosbok OR sitatunga OR taurotragus OR eland OR hippotragus OR sable OR roan OR oryx OR gemsb* OR pelea OR rheb* OR redunca OR reedbuck OR rietbok OR "kobus ellipsiprymnus" OR waterb* OR "kobus leche" OR lechwe OR "kobus kob" OR "kobus vardonii" OR puku OR cephalophus OR sylvicapra OR philantomba OR duiker OR oreotragus OR klipspringer OR spekei OR leptoceros OR "Gazella dorcas" OR eudorcas OR nanger OR addax OR "capra nubiana" OR "nubian ibex" OR beatragus OR hirola OR ammotragus OR "barbary sheep" OR dorcatragus OR madoqua OR "dik-dik" OR okapia OR okapi OR neotragus OR "royal antelope" OR suni OR litocranius OR gerenuk OR hyemoschus OR chevrotain OR ourebia OR oribi) NOT TI (beetle OR arthropod OR oryctes OR nudivirus OR javan OR sumatran OR "one horned" OR snake OR chicken* OR human* OR Newcastle OR arabi* OR tragus OR aquaculture OR waterborne) OR AB (Africa*) AND AB (virus OR viral) AND AB (loxodonta OR "african elephant" OR giraff* OR syncerus OR "african buffalo" OR "cape buffalo" OR hippopotamus OR choeropsis OR rhinoceros OR ceratotherium OR diceros OR "equus zebra" OR "equus africanus" OR grevyi OR quagga OR phacochoerus OR warthog OR potamochoerus OR bushpig OR "red river hog" OR aepyceros OR impala OR alcelaphus OR hartebees* OR connochaetes OR wildebees* OR damaliscus OR tsessebe OR bonteb* OR blesb* OR antidorcas OR springb* OR raphicerus OR steenb* OR grysbok OR tragelaphus OR kudu OR koedoe OR nyala OR bongo OR bushbuck OR bosbok OR sitatunga OR taurotragus OR eland OR hippotragus OR sable OR roan OR oryx OR gemsb*

OR pelea OR rheb* OR redunca OR reedbuck OR rietbok OR "kobus ellipsiprymnus" OR waterb* OR "kobus leche" OR lechwe OR "kobus kob" OR "kobus vardonii" OR puku OR cephalophus OR sylvicapra OR philantomba OR duiker OR oreotragus OR klipspringer OR spekei OR leptoceros OR "Gazella dorcas" OR eudorcas OR nanger OR addax OR "capra nubiana" OR "nubian ibex" OR beatragus OR hirola OR ammotragus OR "barbary sheep" OR dorcatragus OR madoqua OR "dik-dik" OR okapia OR okapi OR neotragus OR "royal antelope" OR suni OR litocranius OR gerenuk OR hyemoschus OR chevrotain OR ourebia OR oribi) NOT AB (beetle OR arthropod OR oryctes OR nudivirus OR javan OR sumatran OR "one horned" OR snake OR chicken* OR human* OR Newcastle OR arabi* OR tragus OR aquaculture OR waterborne) OR KA (Africa*) AND KA (virus OR viral) AND KA (loxodonta OR "african elephant" OR giraff* OR syncerus OR "african buffalo" OR "cape buffalo" OR hippopotamus OR choeropsis OR rhinoceros OR ceratotherium OR diceros OR "equus zebra" OR "equus africanus" OR grevyi OR quagga OR phacochoerus OR warthog OR potamochoerus OR bushpig OR "red river hog" OR aepyceros OR impala OR alcelaphus OR hartebees* OR connochaetes OR wildebees* OR damaliscus OR tsessebe OR bonteb* OR blesb* OR antidorcas OR springb* OR raphicerus OR steenb* OR grysbok OR tragelaphus OR kudu OR koedoe OR nyala OR bongo OR bushbuck OR bosbok OR sitatunga OR taurotragus OR eland OR hippotragus OR sable OR roan OR oryx OR gemsb* OR pelea OR rheb* OR redunca OR reedbuck OR rietbok OR "kobus ellipsiprymnus" OR waterb* OR "kobus leche" OR lechwe OR "kobus kob" OR "kobus vardonii" OR puku OR cephalophus OR sylvicapra OR philantomba OR duiker OR oreotragus OR klipspringer OR spekei OR leptoceros OR "Gazella dorcas" OR eudorcas OR nanger OR addax OR "capra nubiana" OR "nubian ibex" OR beatragus OR hirola OR ammotragus OR "barbary sheep" OR dorcatragus OR madoqua OR "dik-dik" OR okapia OR okapi OR neotragus OR "royal antelope" OR suni OR litocranius OR gerenuk OR hyemoschus OR chevrotain OR ourebia OR oribi) NOT KA (beetle OR arthropod OR oryctes OR nudivirus OR javan OR sumatran OR "one horned" OR snake OR chicken* OR human* OR Newcastle OR arabi* OR tragus OR aquaculture OR waterborne)

9.4. Adapted for Web of Science

TS=Africa* AND TS=(virus OR viral) AND TS=(loxodonta OR “african elephant” OR giraff* OR syncerus OR “african buffalo” OR “cape buffalo” hippopotamus OR choeropsis OR rhinoceros OR ceratotherium OR diceros OR “equus zebra” OR “equus africanus” OR grevyi OR quagga OR phacochoerus OR warthog OR potamochoerus OR bushpig OR “red river hog” OR aepyceros OR impala OR alcelaphus OR hartebees* OR connochaetes OR wildebees* OR damaliscus OR tsessebe OR bonteb* OR blesb* OR antidorcas OR springb* OR raphicerus

OR steenb* OR grysbok OR tragelaphus OR kudu OR koedoe OR nyala OR bongo OR bushbuck OR bosbok OR sitatunga OR taurotragus OR eland OR hippotragus OR sable OR roan OR oryx OR gemsb* OR pelea OR rheb* OR redunca OR reedbuck OR rietbok OR “kobus ellipsiprymnus” OR waterb* OR “kobus leche” OR lechwe OR “kobus kob” OR “kobus vardonii” OR puku OR cephalophus OR sylvicapra OR philantomba OR duiker OR oreotragus OR klipspringer OR spekei OR leptoceros OR "Gazella dorcas" OR eudorcas OR nanger OR addax OR “capra nubiana” OR “nubian ibex” OR beatragus OR hirola OR ammotragus OR "barbary sheep" OR dorcatragus OR madoqua OR "dik-dik" OR okapia OR okapi OR neotragus OR "royal antelope" OR suni OR litocranius OR gerenuk OR hyemoschus OR chevrotain OR ourebia OR oribi) NOT TS=(beetle OR arthropod OR oryctes OR nudivirus OR javan OR sumatran OR “one horned” OR snake OR chicken* OR human* OR Newcastle OR arabian OR tragus OR aquaculture OR waterborne) AND TI=Africa* AND TI=(virus OR viral) AND TI=(loxodonta OR “african elephant” OR giraff* OR syncerus OR “african buffalo” OR “cape buffalo” hippopotamus OR choeropsis OR rhinoceros OR ceratotherium OR diceros OR “equus zebra” OR “equus africanus” OR grevyi OR quagga OR phacochoerus OR warthog OR potamochoerus OR bushpig OR “red river hog” OR aepyceros OR impala OR alcelaphus OR hartebees* OR connochaetes OR wildebees* OR damaliscus OR tsessebe OR bonteb* OR blesb* OR antidorcas OR springb* OR raphicerus OR steenb* OR grysbok OR tragelaphus OR kudu OR koedoe OR nyala OR bongo OR bushbuck OR bosbok OR sitatunga OR taurotragus OR eland OR hippotragus OR sable OR roan OR oryx OR gemsb* OR pelea OR rheb* OR redunca OR reedbuck OR rietbok OR “kobus ellipsiprymnus” OR waterb* OR “kobus leche” OR lechwe OR “kobus kob” OR “kobus vardonii” OR puku OR cephalophus OR sylvicapra OR philantomba OR duiker OR oreotragus OR klipspringer OR spekei OR leptoceros OR "Gazella dorcas" OR eudorcas OR nanger OR addax OR “capra nubiana” OR “nubian ibex” OR beatragus OR hirola OR ammotragus OR "barbary sheep" OR dorcatragus OR madoqua OR "dik-dik" OR okapia OR okapi OR neotragus OR "royal antelope" OR suni OR litocranius OR gerenuk OR hyemoschus OR chevrotain OR ourebia OR oribi) NOT TI=(beetle OR arthropod OR oryctes OR nudivirus OR javan OR sumatran OR “one horned” OR snake OR chicken* OR human* OR Newcastle OR arabian OR tragus OR aquaculture OR waterborne)

10. Appendix C: Ethics approval

UNIVERSITEIT VAN PRETORIA
UNIVERSITY OF PRETORIA
YUNIBESITHI YA PRETORIA

Research Ethics Committee

PROJECT TITLE	**A Systematic Review and Meta-Analysis of Viral Diseases of African Ungulates and Carnivores**
PROJECT NUMBER	**REC043-18**
RESEARCHER/PRINCIPAL INVESTIGATOR	**Hendrik Swanepoel**

DISSERTATION/THESIS SUBMITTED FOR	**MSc**

SUPERVISOR	**Prof Melvyn Quan**

APPROVED	Date **4 July 2018**
CHAIRMAN: UP Research Ethics Committee	Signature A.M. Duncan